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SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
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If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

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Searcher: _____

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Date Searcher Picked Up: 3/26/03

Date Completed: 3/26/03

Searcher Prep & Review Time: _____

Clerical Prep Time: 10

Online Time: 10

Type of Search

NA Sequence (#) _____

AA Sequence (#) ☒

Structure (#) _____

Bibliographic _____

Litigation _____

Fulltext _____

Patent Family _____

Other _____

Vendors and cost where applicable

STN _____

Dialog _____

Questel/Orbit _____

Dr.Link _____

Lexis/Nexis _____

Sequence Systems ☒

WWW/Internet _____

Other (specify) _____

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 07:31:10 ; Search time 11 Seconds
(without alignments)
942.644 Million cell updates/sec

Title: US-09-724-341-8
Perfect score: 1304
Sequence: 1 MPASSPFLAPKPPGNMG.....RARKLNLSPHGFLGFVKL 250

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
al number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1304	100.0	250	1 TN13_HUMAN	O75888 homo sapien
2	1014.5	77.8	241	1 TN13_MOUSE	O9d777 mus musculu
3	244.5	18.8	285	1 T13B_HUMAN	O9y275 homo sapien
4	234.5	18.0	309	1 T13B_MOUSE	O9wu72 mus musculu
5	131	10.0	391	1 EDA_BOVIN	O9beg5 bos taurus
6	131	10.0	391	1 EDA_HUMAN	O92838 homo sapien
7	131	10.0	391	1 EDA_MOUSE	O54693 mus musculu
8	107.5	8.2	234	1 TNFA_CAVPO	P51435 cavia porce
9	105	8.1	235	1 TNFA_RAT	P16599 rattus norv
10	104	8.0	233	1 TNFA_PAPSP	P33620 papio sp. (
11	103.5	7.9	233	1 TNFA_HUMAN	P01375 homo sapien
12	103	7.9	272	1 TNF5_HUMAN	O91868 gallus gall
13	102.5	7.9	235	1 TNFA_RABIT	P04924 oryctolagus
14	102.5	7.9	280	1 TNF6_MACMU	O9my16 macaca mula
15	100	7.7	229	1 TNFA_CEREL	P51743 cervus elap
16	99.5	7.6	235	1 TNFA_MOUSE	P06804 mus musculu
17	99	7.6	233	1 TNFA_BOVIN	O06599 bos taurus
18	98.5	7.6	233	1 TNFA_FELCA	P19101 felis silve
19	98	7.5	233	1 TNFA_MACFA	P48094 macaca fasc
20	98	7.5	233	1 TNFA_MACMU	O77510 papio hamad
21	98	7.5	233	1 TNFA_PAPHU	P29553 equus cabal
22	97.5	7.5	234	1 TNFA_HORSE	O9bdn1 cercocebus
23	97	7.4	280	1 TNF6_CERTO	P50592 mus musculu
24	96.5	7.4	291	1 TN10_MOUSE	P51742 canis fami1
25	95.5	7.3	233	1 TNFA_CANFA	P36939 peromyscus
26	94.5	7.2	235	1 TNFA_PERLE	O8wnr1 delphinapte
27	93	7.1	233	1 TNFA_DELLE	O35734 marmota mon
28	93	7.1	233	1 TNFA_MARMO	P48023 homo sapien
29	93	7.1	281	1 TNF6_HUMAN	O9beal tursiops tr
30	92.5	7.1	233	1 TNFA_TURTR	P36940 rattus norv
31	92.5	7.1	278	1 TNF6_RAT	P23383 ovis aries
32	92	7.1	234	1 TNFA_SHEEP	P13296 capra hircu
33	91.5	7.0	234	1 TNFA_CAPHI	

34	91	7.0	233	1 TNFA_TRIVU	P79374 trichosurus
35	90.5	6.9	583	1 PMEU_LYCES	O41143 lycopersico
36	90	6.9	232	1 TNFA_PIG	P23563 sus scrofa
37	89.5	6.9	205	1 TNFB_HUMAN	P01374 homo sapien
38	89	6.8	282	1 TNF6_PIG	O9bea8 sus scrofa
39	84.5	6.5	364	1 IKBE_MOUSE	O54910 mus musculu
40	83.5	6.4	842	1 PKL2_RAT	O08874 rattus norv
41	83	6.4	260	1 TNF5_FELCA	O97605 felis silve
42	83	6.4	279	1 TNF6_MOUSE	P41047 mus musculu
43	83	6.4	1711	1 PTPO_RAT	O64612 rattus norv
44	82	6.3	197	1 TNFB_RABIT	P10154 oryctolagus
45	81.5	6.2	260	1 TNF5_CANFA	O97626 canis fami1

ALIGNMENTS

RESULT 1
TN13_HUMAN
ID TN13_HUMAN STANDARD; PRT; 250 AA.
AC O75888; Q9P1M8; Q9P1M9; Q96HV6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 13 (A proliferation-inducing ligand) (APRIL) (TNF-and APOU-related leukocyte expressed ligand 2) (TALL-2) (TNF-related death ligand-1) (TRDL-1).
DE ligand 2) (TALL-2) (TNF-related death ligand-1) (TRDL-1).
GN TNFSF13 OR APRIL OR TALL2 OR ZTNF2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=98416181; PubMed=9743536;
RA Hahne M., Kataoka T., Schroeter M., Hofmann K., Imler M., Bodmer J.-L., Schneider P., Bornand T., Holler N., French L.E., Sordet B., Rimoldi D., Techopp J.;
RA "APRIL, a new ligand of the tumor necrosis factor family, stimulates tumor cell growth.";
RT J. Exp. Med. 188:1185-1190(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99260341; PubMed=10331498;
RA Shu H.-B., Hu W.-H., Johnson H.;
RT "TALL-1 is a novel member of the TNF family that is down-regulated by J. Leukoc. Biol. 65:680-683(1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Farrah T., Grant F., Haldeman B., Whitmore T., Gross J., O'Hara P.;
RT "Homo sapiens tumor necrosis factor homolog.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA, BETA AND GAMMA).
RX MEDLINE=20168636; PubMed=10706119;
RA Kelly K.A., Manos E.J., Jensen G.T., Nadault L., Jones D.A.;
RT "APRIL/TRDL-1, a tumor necrosis factor-like ligand, stimulates cell death.";
RL Cancer Res. 60:1021-1027(2000).
RN [5]
RP SEQUENCE OF 1-247 FROM N.A.
RC TISSUE=Ovary;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [6]
RP FUNCTION.
RX MEDLINE=21170294; PubMed=10973284;
RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M.J., Ramakrishnan M., McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M., Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E.;
RA "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating

170

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RT humoral immunity.";
RL Nat. Immunol.1:252-256(2000).
RP PROCESSING BY FURIN, MUTAGENESIS OF ARG-101 AND ARG-104, AND
SUBCELLULAR LOCATION.
RX PubMed=11571266;
RA Lopez-Fraga M., Fernandez R., Albar J.P., Hahne M.;
RT "Biologically active APRIL is secreted following intracellular
processing in the Golgi apparatus by furin convertase.";
RL EMBO Rep. 2:945-951(2001).
CC -1- FUNCTION: Cytokine that binds to TNFRSF13B/TACI and to
TNFRSF17/BCMA. May be implicated in the regulation of tumor cell
growth. May be involved in monocyte/macrophage-mediated
immunological processes.
CC -1- SUBUNIT: Homotrimer (Potential).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALTERNATIVE PRODUCTS: 3 isoforms; ALPHA (SHOWN HERE), BETA AND
GAMMA: ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN TRANSFORMED CELL
LINES, CANCERS OF COLON, THYROID, LYMPHOID TISSUES AND
SPECIFICALLY EXPRESSED IN MONOCYTES AND MACROPHAGES.
CC -1- INDUCTION: DOWN-REGULATED BY PHORBOL MYRISTATE ACETATE/IONOMYCIN
TREATMENT.
CC -1- PTM: The precursor is cleaved by furin.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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DR EMBL; AF046888; AAC61312.1; -
DR EMBL; AF136294; AAD29422.1; -
DR EMBL; AF184972; AAF01321.1; -
DR EMBL; AF114011; AAF59828.1; -
DR EMBL; AF114012; AAF59829.1; -
DR EMBL; AF114013; AAF59830.1; -
DR EMBL; BC008042; AAH08042.1; -
DR Genew; HGNC:11928; TNFSF13.
DR MIM; 604472; -.
DR InterPro; IPR000478; TNF_family.
DR pfam; PF00229; TNF_1.
DR SMART; SMO0207; TNF_1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
DR Cytokine; Cytotoxin; Immune response; Glycoprotein;
Alternative splicing.
FT CHAIN 1 104
FT CHAIN 105 250
TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
MEMBER 13.
CLEAVAGE (BY FURIN).
POTENTIAL.
N-LINKED (GLCNAC. .) (POTENTIAL).
KQSHVLHPINATSKD -> N (IN ISOFORM BETA).
MISSING (IN ISOFORM GAMMA).
RKRR->AKRA: ABOLISHES PROTEOLYTIC
PROCESSING.
FT FT N -> S (IN REF. 5).
FT FT F -> L (IN REF. 5).
FT CONFLICT 96 96
FT CONFLICT 247 247
SQ SEQUENCE 250 AA; 27433 MW; AE1A6B9457FE298 CRC64;
Query Match 100.0%; Score 1304; DB 1; Length 250;
Best local Similarity 100.0%; Pred. No. 9.4e-108;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY	61	EVSRLQGTGSPQNGEGYPWQSLPEQSSDALLEAWENGERSRKRRAVLTQKQKHSHVLHL	120
OY	121	VPINATSKDDSDVTEVMWPALRRRGLOAQGYGVRIQDAGVYLVSQVLFQDYFTTGMQ	180
Dd	121	VPINATSKDDSDVTEVMWPALRRRGLOAQGYGVRIQDAGVYLVSQVLFQDYFTTGMQ	180
OY	181	VVSREGGROETLFRICIRSMPSHPDRAYNSCYSAGVFHLSHQGLISVIIIPRARKLNLSLP	240
Dd	181	VVSREGGROETLFRICIRSMPSHPDRAYNSCYSAGVFHLSHQGLISVIIIPRARKLNLSLP	240
OY	241	HGTFLGFVKL 250	
Dd	241	HGTFLGFVKL 250	
RESULT 2			
ID	TN13_MOUSE	STANDARD;	PRT; 241 AA.
AC	O9D777; Q9ERPL;		
DT	15-JUN-2002 (Rel. 41, Created)		
DT	15-JUN-2002 (Rel. 41, Last sequence update)		
DE	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Tumor necrosis factor ligand superfamily member 13 (A proliferation-inducing ligand) (APRIL).		
GN	TNFSF13 OR APRIL.		
OC	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCHI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Lung;		
RX	MEDLINE=21170294; PubMed=10973284;		
RA	Yu G., Boone T., Delaney J., Hawkins N., Kelley M.J., Ramakrishnan M.		
RA	Mccabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolinska M.,		
RA	Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E.;		
RT	"APRIL and TALL-I and receptors BCMA and TACI: system for regulating humoral immunity."		
RT	Nat. Immunol. 1:252-256(2000).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=Tongue;		
RX	MEDLINE=21085660; PubMed=11217851;		
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,		
RA	Akakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,		
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,		
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,		
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,		
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,		
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,		
RA	Schröml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,		
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,		
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,		
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,		
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,		
RA	Lions P., Marchionni L., Mashima J., Mazzarelli J., Mommaerts P.,		
RA	Nordone P., Ring B., Ringwald C., Rodriguez I., Sakamoto N.,		
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,		
RA	Suzuki H., Toyooka K., Wang K.H., Welts C., Whitaker C., Wilming L.,		
RA	Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,		
RA	Hayashizaki Y.;		
RT	"Functional annotation of a full-length mouse cDNA collection.";		
RT	Nature 409:685-690(2001).		
CC	-1- FUNCTION: Cytokine that binds to TNFRSF13B/TACI and to		
CC	TNFRSF17/BCMA. May be implicated in the regulation of tumor cell		
CC	growth. May be involved in monocyte/macrophage-mediated		
CC	immunological processes.		
CC	-1- SUBUNIT: Homotrimer (Potential).		
CC	-1- SUBCELLULAR LOCATION: Secreted (By similarity).		
CC	-1- PTM: The soluble form derives from the membrane form by		
CC	proteolytic processing.		
CC	-1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.		

CC -----
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CC -----
DR EMBL; AF294825; AAG22534.1; -
DR EMBL; AK009514; BAB26332.1; -
DR MGD; MGI:1916833; Tnfef13.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KW Cytokine; Cytotoxin; Immune response; Glycoprotein.
FT PROPEP 1 95
FT CHAIN 96 241
 BY SIMILARITY.
 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
 MEMBER 13.
SITE 95 96
DISULFID 187 202
FT CARBOHYD 115 115
FT CONFLICT 120 120
SQ SEQUENCE 241 AA; 26889 MW; 4B96D03BDBC712A4 CRC64;
 MISSING (IN REF. 2).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 POTENTIAL.
 CLEAVAGE (BY FURIN) (BY SIMILARITY).
Query Match 77.8%; Score 1014.5; DB 1; Length 241;
Best Local Similarity 79.6%; Pred. No. 2.8e-82;
Matches 199; Conservative 16; Mismatches 26; Indels 9; Gaps 1;
OY 1 MPASSPFLAPKPPGNMGVPREPALSVALLWSGALGAVACAMALLTQOTELQSLRR 60
Db 1 MPASS-----PGHMGSVREPALSVALLWSGAVLGAVTCAVALLIQOTELQSLRR 51
OY 61 EVSRLQGTGSPSQNGEGYPWQSLPEQSSDALAEWNGERSRKRAVLTQKKKHSVLHL 120
Db 52 EVSRLQRSQSPQKQGERPQWQSLPEQSSDVLAEWKDGAKSRRAVLTQKKKHSVLHL 111
OY 121 VPINATSKDSDVTEVMQPALRRGRLQAGYGVRIQDAGVYLYSQVLFDVFTMGQ 180
Db 112 VPVNITSKADSDVTEVMQPVLRKRGLEAQGDIVRWDTGIYLYSQVLFHDVFTMGQ 171
OY 181 VVSREGQROETLFRFCIRSMPSHDPRAVNSCVSAGVFHLHQDILSVIIPRAKINLSP 240
Db 172 VVSREGQRRFTRCIRSMPSDPRAYNSCVSAGVFHLHQDITTVKIPRANAKLSLSP 231
241 HGTFLGFVKL 250
232 HGTFLGFVKL 241
RESULT 3
T13B_HUMAN
ID T13B_HUMAN STANDARD; PRT; 285 AA.
AC Q9Y275;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 13B (TNF-and APOL-
DE related leukocyte expressed ligand 1) (TALL-1) (B lymphocyte
DE stimulator) (Blys) (B cell-activating factor) (BAFF) (Dendritic cell-
DE derived TNF-like molecule).
GN TNFSF13B OR TALL1 OR Blys OR BAFF OR ZTNF4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99260341; PubMed=10331498;
RA Shu H.-B., Hu W.-H., Johnson H.;
RT "TALL-1 is a novel member of the TNF family that is down-regulated by

RT mitogens.";
RL J. Leukoc. Biol. 65:680-683(1999).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 134-148.
RX MEDLINE=99288033; PubMed=10359578;
RA Schneider P., Mackay F., Steiner V., Hofmann K., Bodmer J.-L.,
RA Holler N., Ambrose C., Lawton P., Bixler S., Acha-Orbea H.,
RA Valmori D., Romero P., Werner-Favre C., Zubler R.H., Browning J.L.,
RA Tschoopp J.;
RT "BAFF, a novel ligand of the tumor necrosis factor family, stimulates
RT B cell growth.";
RL J. Exp. Med. 189:1747-1756(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Neutrophils, and Monocytes;
RX MEDLINE=99329343; PubMed=10398604;
RA Moore P.A., Belvedere O., Orr A., Pieri K., Lafleur D.W., Feng P.,
RA Soppet D., Chatters M., Gentz R., Parmelee D., Li Y., Galperina O.,
RA Giri J., Roschke V., Nardelli B., Carrell J., Sosnovtseva S.,
RA Greenfield W., Ruben S.M., Olsen H.S., Fikes J., Hilbert D.M.;
RT "Blys: member of the tumor necrosis factor family and B lymphocyte
RT stimulator.";
RL Science 285:260-263(1999).
RN [4]
RP SEQUENCE FROM N.A.
RA Farrah T., Grose J., Piddington C., O'Hara P.;
RT "Homo sapiens homolog of tumor necrosis factor.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Dendritic cell;
RA Zhang W., Wan T., Yu Y., Gao X.;
RT "A novel dendritic cell-derived TNF-like molecule.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE OF 1-135 FROM N.A., AND VARIANT THR-105.
RA Kawasaki A., Tsuchiya N., Fukazawa T., Hashimoto H., Tokunaga K.;
RT "New polymorphisms of human Blys gene.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [8]
RP FUNCTION.
RX MEDLINE=21170294; PubMed=10973284;
RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M.J., Ramakrishnan M.,
RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
RA Boyle W.J., Sarosi I., Hu H., Senaldi G., Theill L.E.;
RT "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating
RT humoral immunity.";
RL Nat. Immunol. 1:252-256(2000).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 142-285.
RX PubMed=11853672;
RA Liu Y., Xu L., Opalka N., Kappler J., Shu H.-B., Zhang G.;
RT "Crystal structure of eTALL-1 reveals a virus-like assembly of TNF
RT family ligands.";
RL Cell 108:383-394(2002).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 136-285.
RX PubMed=11827482;
RA Karpusas M., Cachero T.G., Qian F., Boriack-Sjodin A., Mullen C.,
RA Strauch K., Hsu Y.-M., Kalled S.L.;
RT "Crystal structure of extracellular human BAFF, a TNF family member
RT that stimulates B lymphocytes.";
RL J. Mol. Biol. 315:1145-1154(2002).
RN [11]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 134-285.
RX PubMed=11862220;
RA Oren D.A., Li Y., Volovik Y., Morris T.S., Dharja C., Das K.,
RA Galperina O., Gentz R., Arnold E.;

RT "Structural basis of Blys receptor recognition."
RL Nat. Struct. Biol. 9:288-292(2002).
CC -1- FUNCTION: Cytokine that binds to TNFRSF13B/TACI and TNFRSF17/BCMA.
CC TNFRSF13/APRIL binds to the same 2 receptors. Together, they form a
CC 2 ligands -2 receptors pathway involved in the stimulation of B-
CC and T-cell function and the regulation of humoral immunity. A
CC third B-cell specific BAFR-receptor (BAFR/BR3) promotes the
CC survival of mature B-cells and the B-cell response.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM.
CC -1- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN PERIPHERAL BLOOD
CC LEUCOCYTES AND IS SPECIFICALLY EXPRESSED IN MONOCYTES AND
CC MACROPHAGES. ALSO FOUND IN THE SPLEEN, LYMPH NODE, BONE MARROW, T-
CC CELLS AND DENDRITIC CELLS. A LOWER EXPRESSION SEEN IN PLACENTA,
CC HEART, LUNG, FETAL LIVER, THYMUS, AND PANCREAS.
CC -1- INDUCTION: UPREGULATED BY EXPOSURE TO INTERFERON-GAMMA. DOWN-
CC REGULATED BY PHORBOL MYRISTATE ACETATE/IONOMYCIN TREATMENT.
CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC PROTEOLYTIC PROCESSING.
CC -1- PTM: N-glycosylated.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC -----
DR EMBL; AF136293; AAD29421.1; -
DR EMBL; AF116456; AAD25356.1; -
DR EMBL; AF132600; AAD21092.1; -
DR EMBL; AF186114; AAF01432.1; -
DR EMBL; AF134715; AAF60219.1; -
DR EMBL; AB073225; BAB90856.1; -
DR EMBL; BC020674; AAH20674.1; -
DR PDB; 1KXG; 20-MAR-02.
DR PDB; 1KD7; 12-NOV-02.
DR PDB; 1JH5; 08-FEB-02.
DR Genew; HGNC:11929; TNFRSF13B.
DR MIM; 603969; -
DR InterPro; IPR000478; TNF_family.
DR SMART; SM00207; TNF, 1.
DR PROSITE; PS00251; TNF_1; FALSE_NEG.
DR PROSITE; PS50049; TNF_2; 1.
DR Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor;
DR 3D-structure; Polymorphism.
CHAIN 1 285
FT CHAIN 134 285 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT MEMBER 13B, MEMBRANE FORM.
FT TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT TRANSMEM 47 67 MEMBER 13B, SOLUBLE FORM.
FT CYTOPLASMIC (POTENTIAL).
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT DOMAIN 68 285 EXTRACELLULAR (POTENTIAL).
FT SITE 133 134 CLEAVAGE.
FT DISULFID 232 245
FT CARBOHYD 124 124
FT CARBOHYD 242 242
FT VARIANT 105 105
FT SEQUENCE 285 AA; 31222 MW; 48ED0D7AB38C8867 CRC64;
SO
Query Match 18.8%; Score 244.5; DB 1; Length 285;
Best Local Similarity 29.7%; Pred. No. 2.3e-14;
Matches 70; Conservative 47; Mismatches 90; Indels 29; Gaps 8;
QY 39 LGAVACAMALLT-----QOTELQSLREVSRLQGTGSPSONGEGYPWQSLPEQS--SDA 90
DB 54 LALLSCLTVVSFYQVAAALQGDLASLRALQGHAAEKLPAA--GAGAPKAGLEAPAVTAG 111

QY 91 LEAWE-----NGERSRKRRAVLTKOKKOHSLHLVLPINAT-SKDDSDVTEVMQPA 141
DB 112 LKIFEPAPGEGNSSQNSRNKRAVQPEETVTQDCLQLIADSETPTIQKGYTFVPWLLS 171
QY 142 LRRGRGLQAGYGVRIQDAGVLLYSQVLFQDVTFTMGQVVSRE-----GQGRQETLFR 195
DB 172 FRGSALBEKENKILVKETGYFFIYGQVLYDKTYAMGHLIQKKVHVFGDELSVTLFR 231
QY 196 CIRSMPSHPDRAVNSCYSGVFLHOGDILSVIIPARAKNLSPHGTFLEFVKL 250
DB 232 CIQMPETLPN--NSCYSAGIAKLEEGDELQALPRENAQISLDGDVTFFGALKL 284
RESULT 4
T13B_MOUSE
ID T13B_MOUSE STANDARD; PRT; 309 AA.
AC Q9WU72;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 13B (B cell-activating
DE factor) (BAFF).
GN TNFRSF13B OR BAFB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99288033; PubMed=10359578;
RA Schneider P., Mackay F., Steiner V., Hofmann K., Bodmer J.-L.,
RA Holler N., Ambrose C., Lawton P., Bixler S., Acha-Orbea H.,
RA Valmori D., Romero P., Werner-Favre C., Zuhler R.H., Browning J.L.,
RA Tschoopp J.;
RT "BAFF, a novel ligand of the tumor necrosis factor family, stimulates
RT B cell growth."
RL J. Exp. Med. 189:1747-1756(1999).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANT SER-79.
RC STRAIN=N2B;
RX PubMed=11862414;
RA Jiang Y., Ohtsui M., Abe M., Li N., Xiu Y., Wen X.S., Shirai T.,
RA Hirose S.;
RT "Polymorphism and chromosomal mapping of the mouse gene for B-cell
RT activating factor belonging to the tumor necrosis factor family
RT (Baff) and association with the autoimmune phenotype."
RL Immunogenetics 53:810-813(2001).
CC -1- FUNCTION: Cytokine that binds to TNFRSF13B/TACI and TNFRSF17/BCMA.
CC TNFRSF13/APRIL binds to the same 2 receptors. Together, they form a
CC 2 ligands -2 receptors pathway involved in the stimulation of B-
CC and T-cell function and the regulation of humoral immunity. A
CC third B-cell specific BAFR-receptor (BAFR/BR3) promotes the
CC survival of mature B-cells and the B-cell response.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM.
CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC PROTEOLYTIC PROCESSING.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC -----
DR EMBL; AF119383; AAD22475.1; -
DR EMBL; AF352245; AAL83939.1; -
DR MGD; MGI:1344376; Tnfsl13b.
DR InterPro; IPR000478; TNF_family.
DR SMART; SM00207; TNF, 1.

Query Match	Best Local Similarity	Score 234.5; DB 1; Length 309;
Matches 82; Conservative 44; Mismatches 104; Indels 61; Gaps 11;		
DR PROSITE; PS00251; TNF_1; FALSE_NEG.		
DR PROSITE; PS50049; TNF_2; 1.		
KW Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor;		
KM Polymorphism.		
FT CHAIN 1 309		TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 13B, MEMBRANE FORM.
FT CHAIN 127 309		TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 13B, SOLUBLE FORM.
FT DOMAIN 1 47		CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 48 68		SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
FT DOMAIN 69 309		EXTRACELLULAR (POTENTIAL).
FT SITE 126 127		CLEAVAGE (BY SIMILARITY).
FT DISULFID 256 269		BY SIMILARITY.
FT CARBOHYD 117 117		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 266 266		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 79 79		N -> S (IN STRAIN NZB).
SO SEQUENCE 309 AA; 34192 MW; F3DE6056E6034B4 CRC64;		

RESULT 5	EDNA_BOVIN	EDNA_BOVIN	STANDARD;	PRT;	391 AA.
ID	EDNA_BOVIN				
Q9BEG5; Q9BEG6;					
15-JUN-2002 (Rel. 41, Created)					
15-JUN-2002 (Rel. 41, Last sequence update)					
15-JUN-2002 (Rel. 41, Last annotation update)					
DE Ectodysplasin A (Ectodysplasin 1) (Ectodermal dysplasia protein).					
GN ED1 OR EDA.					
OS Bos taurus (Bovine).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;					
OC Bovidae; Bovinae; Bos.					
OX NCBI_TaxID=9913;					
RN [1]					
RP SEQUENCE FROM N.A. (ISOFORMS A1 AND A2).					
RC STRAIN=Holstein;					
RX PubMed=11167539;					
RA Droegemeier C., Distl O., Leeb T.;					
RT "Identification of a highly polymorphic microsatellite within the					
RL bovine ectodysplasin A (ED1) gene on BTA Xq22-24.";					
Anim. Genet. 31:416-416(2000).					
CC -1- FUNCTION: Probably involved in epithelial-mesenchymal signaling.					
CC Isoform A1 binds only to the receptor EDAR, while isoform A2 binds					
CC exclusively to the receptor XEDAR (By similarity).					
CC -1- SUBUNIT: Homotrimer (By similarity).					
CC -1- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By					
CC similarity).					
CC -1- ALTERNATIVE PRODUCTS: At least 2 isoforms; A1 (shown here) and A2;					

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CC      are produced by alternative splicing.
CC      -|- PTM: N-glycosylated (By similarity).
CC      -|- PTM: Processing by furin produces a secreted form (By similarity).
CC      -|- DISEASE: Defects in ED1 are the cause of anhidrotic ectodermal
CC      dysplasia. The disease is characterized by sparse hair (atrichosis
CC      or hypotrichosis), abnormal or missing teeth and the inability to
CC      sweat due to the absence of sweat glands.
CC      -|- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC      -----
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CC	-----	
DR	EMBL; AJ300468; CAC29151.1; .	JOINED.
DR	EMBL; AJ300469; CAC29151.1; .	JOINED.
DR	EMBL; AJ278907; CAC29151.1; .	JOINED.
DR	EMBL; AJ300468; CAC29152.1; .	JOINED.
DR	EMBL; AJ300469; CAC29152.1; .	JOINED.
DR	EMBL; AJ278907; CAC29152.1; .	JOINED.
DR	InterPro; IPR000087; Collagen.	
DR	InterPro; IPR000478; TNF_family.	
DR	SMART; SM00207; TNF; 1.	
DR	PROSITE; PS00251; TNF_1; FALSE_NEG.	
DR	PROSITE; PS50049; TNF_2; 1.	
KW	developmental protein; Differentiation; Transmembrane; Signal-anchor; Glycoprotein; Alternative splicing.	
FT	CHAIN 1 391	ECTODYSPLASIN A, MEMBRANE FORM.
FT	CHAIN 160 391	ECTODYSPLASIN A, SECRETED FORM (BY SIMILARITY).
FT	DOMAIN 1 41	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 42 62	SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
FT	DOMAIN 63 391	EXTRACELLULAR (POTENTIAL).
FT	SITE 159 160	CLEAVAGE (BY FURIN) (BY SIMILARITY).
FT	DOMAIN 180 229	COLLAGEN-LIKE.
FT	CARBOHYD 313 313	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 372 372	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC 307 306	MISSING (IN ISOFORM A2).
SEQ	SEQUENCE 391 AA; 41567 MW; 1F87AD67A04EB7AA CRC64;	

	Query Match	10.0%	Score 131;	DB 1;	Length 391;
	Best Local Similarity	23.2%	Pred. No. 0.00035;		
	Matches 58; Conservative	34;	Mismatches 100;	Indels 58;	Gaps 9;

OY	11 PKGPPGNMG--GPVREPALSVALWLSWGALGAIVACAMALLTQOTELQSRLREVSRLOGT	68
	: :	
DB	184 PNGPPGPPRPGPPGGPPGIPGIPGIPGTVMGP-----PGR	219
OY	69 GCPSPNGEGYPWQSLPEQSSDALEAWENGERSRRKRAVLTKOKKHSHLVLPINAT--	126
	: : : : :	: : :
DB	220 PGP-PGPQRPGLQGPPSGAADKAKGTREN-----QPAVNHLCGGSAIQ	261
OY	127 SKDD-----SDYTEVWMQPALARRGRLQAQGYVRIODAGVLLYSQVLFQDVFPTMGQ	180
	: : : : : :	: : : :
DB	262 VKNDLSGVLDMSRITMNPKVFK---LHPRSGELEVLVDGTVPFIYSQVEVVYNFT--D	316
OY	181 VVSREGQGRQETLFRICIRSMPSHDRAVNSCYSGAVFHLHQGDILSVIIPARAKNLSP	240
	: : : : : : : : : :	: : : : : : : :
DB	317 FASYEVVVDDEKPLQCTRSIETGKTN-YNTCYTAGVCCLKARQKIAVKMVHADISINMSK	375
OY	241 HGTELGFWKL	250
	: :	
DB	376 HTTFEFGAIRL	385

RESULT	6
ID_EDA_HUMAN	STANDARD; PRT; 391 AA.
AC	Q9Z838; Q75910; Q9UP77; Q9Y6L0; Q9Y6L1; Q9Y6L2; Q9Y6L3; Q9Y6L4; Q9Z838; Q75910; Q9UP77; Q9Y6L0; Q9Y6L1; Q9Y6L2; Q9Y6L3; Q9Y6L4;

DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ectodysplasin A (Ectodermal dysplasia protein) (EDA protein).
GN ED1 OR EDA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM I), AND VARIANTS EDA HIS-61 AND LEU-69.
RC TISSUE=Sweat gland;
RX MEDLINE=96331280; PubMed=8696334;
RA Kere J., Srivastava A.K., Montonen O., Zonana J., Thomas N.S.T.,
RA Ferguson B.M., Munoz F., Morgan D., Clarke A., Baydayan P.,
RA Chen E.Y., Ezer S., Saarialho-Kere U., Ia Chapelle A.,
RA Schlessinger D.;
RT "X-linked anhidrotic (hypohidrotic) ectodermal dysplasia is caused by
RT mutation in a novel transmembrane protein.";
RL Nat. Genet. 13:409-416(1996).
RL [2]
RN SEQUENCE FROM N.A. (ISOFORM A1), AND VARIANTS EDA.
RC TISSUE=Liver;
RX MEDLINE=96349961; PubMed=9683615;
RA Montreal A.W., Zonana J., Ferguson B.M.;
RT "Identification of a new splice form of the EDAl gene permits
RT detection of nearly all X-linked hypohidrotic ectodermal dysplasia
RT mutations.";
RL Am. J. Hum. Genet. 63:380-389(1998).
RL [3]
RN SEQUENCE FROM N.A. (ISOFORMS A1; A2; B; C; D; E AND F), AND VARIANTS
RP EDA.
RX MEDLINE=98409495; PubMed=9736768;
RA Bayers M., Hartung A.J., Ezer S., Pispas J., Thesleff I.,
RA Srivastava A.K., Kere J.;
RT "The anhidrotic ectodermal dysplasia gene (EDA) undergoes alternative
RT splicing and encodes ectodysplasin-A with deletion mutations in
RT collagenous repeats.";
RL Hum. Mol. Genet. 7:1661-1669(1998).
RL [4]
RN SEQUENCE FROM N.A. (ISOFORMS A1 AND C).
RP Clark S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP TISSUE SPECIFICITY, AND ALTERNATIVE SPLICING.
RA Kobiela K., Kobiela A., Trzcielak W.H.;
RT "Expression of a novel transcript isoform of the EDA gene in human
RT umbilical cord.";
RL Eur. J. Hum. Genet. Suppl. 7:104-104(1999).
RN [6]
RP RECEPTOR INTERACTION (ISOFORMS A1 AND A2).
RX MEDLINE=20495245; PubMed=11039935;
RA Yan M., Wang L.-C., Hymowitz S.G., Schilbach S., Lee J., Goddard A.,
RA de Vos A.M., Gao W.-Q., Dixit V.M.;
RT "Two-amino acid molecular switch in an epithelial morphogen that
RT regulates binding to two distinct receptors.";
RL Science 290:523-527(2000).
RL [7]
RN PROCESSING, MUTAGENESIS OF ARG-153, AND CHARACTERIZATION OF VARIANT
RP H-156.
RX PubMed=11309369;
RA Elomaa O., Pulkkinen K., Hannellius U., Mikola M., Saarialho-Kere U.,
RA Kere J.;
RT "Ectodysplasin is released by proteolytic shedding and binds to the
RT EDAR protein.";
RL Hum. Mol. Genet. 10:953-962(2001).
RL [8]
RN CHARACTERIZATION OF VARIANTS C-155; C-156 AND H-156, MUTAGENESIS OF
RP ARG-153; ARG-158 AND ARG-159, AND CLEAVAGE SITE.
RX PubMed=11416205;
RA Chen Y., Molloy S.S., Thomas L., Gambee J., Baechinger H.P.,
RA Ferguson B.M., Zonana J., Thomas G., Morris N.P.;
RT "Mutations within a furin consensus sequence block proteolytic release

RT of ectodysplasin-A and cause X-linked hypohidrotic ectodermal
RT dysplasia.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:7218-7223(2001).
RN [9]
RP VARIANT EDA TYR-54.
RX MEDLINE=98292028; PubMed=9630076;
RA Hertz J.M., Noergaard Hansen K., Juncker I., Kjeldsen M.,
RA Gregersen N.;
RT "A novel missense mutation (402C->T) in exon 1 in the EDA gene in a
RT family with X-linked hypohidrotic ectodermal dysplasia.";
RL Clin. Genet. 53:205-209(1998).
RN [10]
RP VARIANT EDA LYS-63.
RX MEDLINE=98168231; PubMed=9507389;
RA Ferguson B.M., Thomas N.S.T., Munoz F., Morgan D., Clarke A.,
RA Zonana J.;
RT "Scarcity of mutations detected in families with X linked hypohidrotic
RT ectodermal dysplasia: diagnostic implications.";
RL J. Med. Genet. 35:112-115(1998).
RN [11]
RP VARIANT EDA ARG-55.
RX MEDLINE=99399307; PubMed=10469321;
RA Martinez F., Millan J.M., Orellana C., Prieto F.;
RT "X-linked anhidrotic (hypohidrotic) ectodermal dysplasia caused by a
RT novel mutation in EDAl gene: 406T > G (Leu55Arg).";
RL J. Invest. Dermatol. 113:285-286(1999).
RN [12]
RP VARIANTS EDA R-60; Y-252; V-269; S-302 AND M-378.
RX PubMed=11378824;
RA Vincent M.C., Biancalana V., Ginisty D., Mandel J.L., Calvas P.;
RT "Mutational spectrum of the ED1 gene in X-linked hypohidrotic
RT ectodermal dysplasia.";
RL Eur. J. Hum. Genet. 9:355-363(2001).
RN [13]
RP VARIANTS EDA C-156; H-156; C-255; D-255; G-274; Y-332 AND T-349.
RX MEDLINE=21193173; PubMed=11295832;
RA Paeackkoenen K., Cambiaghi S., Novelli G., Ouzts L.V., Penttinen M.,
RA Kere J., Srivastava A.K.;
RT "The mutation spectrum of the EDA gene in X-linked anhidrotic
RT ectodermal dysplasia.";
RL Hum. Mutat. 17:349-349(2001).
RL [14]
RP FUNCTION: Seems to be involved in epithelial-mesenchymal signaling
CC during morphogenesis of ectodermal organs. Isoform A1 binds only
CC to the receptor EDAR, while isoform A2 binds exclusively to the
CC receptor XEDAR.
CC [15]
CC SUBUNIT: Homotrimer.
CC [16]
CC SUBCELLULAR LOCATION: Type II membrane protein and secreted.
CC [17]
CC ALTERNATIVE PRODUCTS: At least 8 isoforms; I, A1/I1 (shown here),
CC A2, B, C, D, E and F; are produced by alternative splicing.
CC [18]
CC TISSUE SPECIFICITY: NOT ABUNDANT; EXPRESSED IN SPECIFIC CELL TYPES
CC OF ECTODERMAL (BUT NOT MESODERMAL) ORIGIN OF KERATINOCYTES, HAIR
CC FOLLICLES, SWEAT GLANDS. ALSO IN ADULT HEART, LIVER, MUSCLE,
CC PANCREAS, PROSTATE, FETAL LIVER, UTERUS, SMALL INTESTINE AND
CC UMBILICAL CHORD.
CC [19]
CC PTM: N-glycosylated.
CC [20]
CC PTM: Processing by furin produces a secreted form.
CC [21]
CC DISEASE: DEFECTS IN ED1 ARE THE CAUSE OF X-LINKED ANHIDROTIC
CC (HYPOHIDROTIC) ECTODERMAL DYSPLASIA (XLHD OR EDA); A DISEASE
CC CHARACTERIZED BY SPARSE HAIR (ATRICHOSIS OR HYPOTRICHOSIS),
CC ABNORMAL OR MISSING TEETH AND THE INABILITY TO SWEAT DUE TO THE
CC ABSENCE OF SWEAT GLANDS. EDA IS THE MOST COMMON FORM OF OVER 150
CC CLINICALLY DISTINCT ECTODERMAL DYSPLASIAS. THIS DISEASE WAS
CC ALREADY DESCRIBED BY DARWIN.
CC [22]
CC SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC [23]
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CC -----

DR	EMBL; AF016627; AAB95202.1; -.
DR	EMBL; AF016628; AAB95203.1; -.
DR	EMBL; AF016629; AAB95204.1; -.
DR	EMBL; AF016630; AAB95205.1; -.
DR	EMBL; AF016631; AAB95206.1; -.
DR	EMBL; AF004434; AAB88121.1; -.
DR	EMBL; AF004435; AAB88122.1; -.
DR	EMBL; Y13438; CAA73849.1; -.
DR	EMBL; AJ243657; CAB52696.1; -.
DR	EMBL; AJ243658; CAB52697.1; -.
DR	MGD; MGI:1195272; Eda.
DR	InterPro; IPR000087; Collagen.
DR	pfam; PF01391; Collagen; 1.
DR	SMART; SMO0207; TNF_1.
DR	PROSITE; PS00251; TNF_1; FALSE_NEG.
DR	PROSITE; PSS0049; TNF_2; 1.
KW	Developmental protein; Differentiation;
KW	Signal-anchor; Glycoprotein; Alternative splicing.
FT	CHAIN 1 391 CHAIN 160 391 ECTODYSPLASIN A, SECRETED FORM (BY SIMILARITY).
FT	DOMAIN 1 41 TRANSMEM 42 62 CYTOPLASMIC (POTENTIAL). SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
FT	EXTRACELLULAR (POTENTIAL). COLLAGEN-LIKE. CLEAVAGE (BY FURIN) (BY SIMILARITY). N-LINKED (GLCNAC. . .) (POTENTIAL). N-LINKED (GLCNAC. . .) (POTENTIAL). MALINFEEPEKAYSEESRRVRNRKRSGEGADGPVKNKKKGGKAGPCPGNGRPPGCPGQPGPIPGIPCTVTMGPDPGPPGQPPGLGPSGA -> VSHLGGAALEAPSPALGGGLGLRAQGTLPRAKFQGRSMEWAGVLGRCCPGVVLGSCLGSSRPSPVPWSWKQAQPARAPEGVWAA (IN ISOFORM TAC).
FT	PVKNRKKKG -> KSTQVIFFP (IN ISOFORM TAB). MISSING (IN ISOFORM TAB). MISSING (IN ISOFORM TAC). MISSING (IN ISOFORM TA-A3). MISSING (IN ISOFORM TAD). MISSING (IN ISOFORM TA-A2 AND ISOFORM TA-A3).
FT	CONFLICT 126 126 SEQUENCE 391 AA; 41603 MW; D -> E (IN REF. 2). ESECEDASBD60DEFF CRC64;

Query Match	10.0%;	Score 131;	DB 1;	Length 391;
Best Local Similarity	23.2%;	Pred. No. 0.00035;		
Matches 58;	Conservative 34;	Mismatches 100;	Indels 58;	Gaps 9;

[illegible]

RESULT 8	
TNFA_CAVPO	
ID_TNFA_CAVPO	STANDARD;
	PRT;
	234 AA

```

AC P51435;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE ligand superfamily member 2) (Cachectin).
GN TNF OR TNFSF2 OR TNFA.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Hartley; TISSUE=Lung;
RA Yuan H.T., Kelly F.J., Bingle C.D.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Dunkin-Hartley;
RX MEDLINE=97462215; PubMed=9316485;
RA White A.M., Yoshimura T., Smith A.W., Westwick J., Watson M.L.;
RT "Airway inflammation induced by recombinant guinea pig tumor necrosis
RT factor-alpha.";
RL Am. J. Physiol. 273:L524-L530(1997).
CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
CC induce cell death of certain tumor cell lines. It is potent
CC pyrogen causing fever by direct action or by stimulation of
CC interleukin 1 secretion and is implicated in the induction of
CC cachexia, Under certain conditions it can stimulate cell
CC proliferation and induce cell differentiation.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -1- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -1- PTM: The membrane form, but not the soluble form, is
CC phosphorylated on serine residues. Dephosphorylation of the
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC similarity).
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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DR EMBL; U39839; AAB06492.1; -
DR EMBL; U77036; AAB19210.1; -
DR HSSP; P06804; 2TNF.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PRO1234; TNECROSISFCT.
DR ProDom; PD002012; TNF_abc; 1.
DR SMART; SMO0207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KW Cytokine; Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor.
FT CHAIN 1 234
FT DOMAIN 80 234 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 57 234 EXTRACELLULAR (POTENTIAL).
FT SITE 79 80 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
FT MOD RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).

```


RT "Cloning and expression in *Escherichia coli* of the gene for human
 RT tumour necrosis factor.";
 RL Nature 313:803-806(1985).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86016093; PubMed=2995927;
 RA Nedwin G.E., Naylor S.L., Sakaguchi A.Y., Smith D.H.,
 RA Jarrett-Nedwin J., Pennica D., Goeddel D.V., Gray P.W.;
 RT "Human lymphotoxin and tumor necrosis factor genes: structure,
 RT homology and chromosomal localization.";
 RL Nucleic Acids Res. 13:6361-6373(1985).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85142190; PubMed=3856324;
 RA Wang A.M., Creasey A.A., Lachner M.B., Lin L.S., Strickler J.,
 RA van Arsdale J.N., Yamamoto R., Mark D.F.;
 RT "Molecular cloning of the complementary DNA for human tumor necrosis
 RT factor.";
 RL Science 228:149-154(1985).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86030296; PubMed=3932069;
 RA Marmenout A., Fransen L., Tavernier J., van der Heyden J., Tizard R.,
 RA Kawashima E., Shaw A., Johnson M.J., Semon D., Mueller R.,
 RA Ruysschaert M.R., van Vliet A., Fiers W.;
 RT "Molecular cloning and expression of human tumor necrosis factor and
 RT comparison with mouse tumor necrosis factor.";
 RL Eur. J. Biochem. 152:515-522(1985).
 RN [7]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93272029; PubMed=8499947;
 RA Iris F.J.M., Bougueleret L., Prieur S., Caterina D., Primas G.,
 RA Perrot V., Jurka J., Rodriguez-Tome P., Claverie J.-M., Dausset J.,
 RA Cohen D.;
 RT "Dense Alu clustering and a potential new member of the NF kappa B
 RT family within a 90 kilobase HLA class III segment.";
 RL Nat. Genet. 3:137-145(1993).
 RN [8]
 RP SEQUENCE FROM N.A.
 RA Rowen L., Madan A., Qin S., Shaffer T., James R., Ratcliffe A.,
 RA Abbasi N., Dickhoff R., Loretz C., Madan A., Dors M., Young J.,
 RA Laaky S., Hood L.;
 RT "Sequence of the human major histocompatibility complex class III
 RT region.";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP SEQUENCE FROM N.A.
 RA Shina S., Tamiya G., Oka A., Inoko H.;
 RT "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [10]
 RP SEQUENCE FROM N.A.
 RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
 RA Nickerson D.A.;
 RT Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 RN [11]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RA Strausberg R.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 RN [12]
 RP PHOSPHORYLATION (MEMBRANE FORM).
 RX PubMed=8597870;
 RA Pocsis E., Duda E., Wallach D.;
 RT "Phosphorylation of the 26 kDa TNF precursor in monocytic cells and in
 RT transfectected HeLa cells.";
 RL J. Inflamm. 45:152-160(1995).
 RN [13]
 RP PHOSPHORYLATION BY CK1, AND DEPHOSPHORYLATION.
 RX PubMed=10205166;
 RA Watts A.D., Hunt N.H., Wanigasekara Y., Bloomfield G., Wallach D.,
 RA Roufogalis B.D., Chaudhri G.;
 RT "A casein kinase I motif present in the cytoplasmic domain of members

RT of the tumour necrosis factor ligand family is implicated in 'reverse
 RT signalling'.";
 RL EMBO J. 18:2119-2126(1999).
 RN [14]
 RP MUTAGENESIS.
 RX MEDLINE=91184128; PubMed=2009860;
 RA Ostade X.V., Tavernier J., Prange T., Fiers W.;
 RT "Localization of the active site of human tumour necrosis factor
 RT (htnf) by mutational analysis.";
 RL EMBO J. 10:827-836(1991).
 RN [15]
 RP MYRISTOYLATION.
 RX MEDLINE=93018820; PubMed=1402651;
 RA Stevenson F.T., Burssten S.L., Locksley R.M., Lovett D.H.;
 RT "Myristyl acylation of the tumor necrosis factor alpha precursor on
 RT specific lysine residues.";
 RL J. Exp. Med. 176:1053-1062(1992).
 RN [16]
 RP CLEAVAGE BY ADAM17.
 RX MEDLINE=97186575; PubMed=9034191;
 RA Moss M.L., Jin S.-L.C., Milla M.E., Burkhardt W., Carter H.L.,
 RA Chen W.-J., Clay W.C., Didsbury J.R., Hassler D., Hoffman C.R.,
 RA Kost T.A., Lambert M.H., Leesltzer M.A., McCauley P., McGeehan G.,
 RA Mitchell J., Moyer M., Patel G., Rocque W., Overton L.K., Schoenen F.,
 RA Seaton T., Su J.-L., Warner J., Willard D., Becherer J.D.;
 RT "Cloning of a disintegrin metalloproteinase that processes precursor
 RT tumour-necrosis factor-alpha.";
 RL Nature 385:733-736(1997).
 RN [17]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE=89159409; PubMed=2922050;
 RA Jones E.Y., Stuart D.I., Walker N.P.;
 RT "Structure of tumour necrosis factor.";
 RL Nature 338:225-228(1989).
 RN [18]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE=91193276; PubMed=1964681;
 RA Jones E.Y., Stuart D.I., Walker N.P.;
 RT "The structure of tumour necrosis factor -- implications for
 RT biological function.";
 RL J. Cell Sci. Suppl. 13:11-18(1990).
 RN [19]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
 RX MEDLINE=90008932; PubMed=2551905;
 RA Eck M.J., Sprang S.R.;
 RT "The structure of tumor necrosis factor-alpha at 2.6-A resolution.
 RT Implications for receptor binding.";
 RL J. Biol. Chem. 264:17595-17605(1989).
 RN [20]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF MUTANT ARG-107.
 RX MEDLINE=98147459; PubMed=9488135;
 RA Reed C., Fu Z.Q., Wu J., Xue Y.N., Harrison R.W., Chen M.J.,
 RA Weber I.T.;
 RT "Crystal structure of TNF-alpha mutant R31D with greater affinity for
 RT receptor RI compared with R2.";
 RL Protein Eng. 10:1101-1107(1997).
 RN [21]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF MUTANT M3S.
 RX MEDLINE=98113178; PubMed=9442056;
 RA Cha S.S., Kim J.S., Cho H.S., Shin N.K., Jeong W., Shin H.C.,
 RA Kim Y.-J., Hahn J.H., Oh B.H.;
 RT "High resolution crystal structure of a human tumor necrosis factor-
 RT alpha mutant with low systemic toxicity.";
 RL J. Biol. Chem. 273:2153-2160(1998).
 CC -I- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
 CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
 CC induce cell death of certain tumor cell lines. It is potent
 CC pyrogen causing fever by direct action or by stimulation of
 CC interleukin 1 secretion and is implicated in the induction of
 CC cachexia, Under certain conditions it can stimulate cell
 CC proliferation and induce cell differentiation.
 CC -I- SUBUNIT: Homotrimer.
 CC -I- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN

```
CC EXTRACELLULAR SOLUBLE FORM.
CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC PROTEOLYTIC PROCESSING.
CC -1- PTM: The membrane form, but not the soluble form, is
CC phosphorylated on serine residues. Dephosphorylation of the
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1.
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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CC -----
CC EMBL; X02910; CAA26669.1; -.
Query Match 7.9%; Score 103.5; DB 1; Length 233;
Best Local Similarity 29.0%; Pred. No. 0.048;
Matches 40; Conservative 20; Mismatches 49; Indels 29; Gaps 7;
OY 123 INATSKDDSD--VTEVMWQPAL-----RRGRGLQAGYGV-----IQDAGVYLLYS 167
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 77 VRSSSRTPSDKPAHVAVNPAEQGLQWLNRRANALLANGVELRDNLVVPSEGLYLIYS 136
OY 168 QVLFD-----VFTMGQV-VREGQGRQETLFR--CIRSMPSHPDRA--YNSCVS 213
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 137 QVLFKGGGCPSTHVLTHITISRIAVSYQTKVNLISAIKSPCQRETEPGAELAKPWYBYVL 196
OY 214 AGVFHLHQGDILSVITIPR 231
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 197 GGVFQLEKGDRLSAEINR 214
RESULT 12
TNFS_CHICK
ID TNFS_CHICK STANDARD; PRT; 272 AA.
AC Q918D8;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-
  l) (CD154 protein).
  TNFSF5 OR CD40LG OR CD40L.
  Gallus gallus (Chicken).
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
  OC Gallus.
  OC NCBI_TaxID=9031;
  OX NCBI_TaxID=9031;
  RN [1]
  RP SEQUENCE FROM N.A.
  RC STRAIN=White leghorn; TISSUE=Spleen;
  RA Tregaskes C.A., Young J.R., Burnside J.;
  RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
  CC -1- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell
  CC proliferation in the absence of co-stimulus as well as IgE
  CC production in the presence of IL-4. Involved in immunoglobulin
  CC class switching (By similarity).
  CC -1- SUBUNIT: Homotrimer (By similarity).
  CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
  CC extracellular soluble form (By similarity).
  CC -1- PTM: The soluble form derives from the membrane form by
  CC proteolytic processing (By similarity).
  CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
  -----
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CC -----
CC EMBL; AJ243435; CAB95748.1; -.
CC HSSP; P29965; ITALY.
CC DR InterPro; IPR003263; TNF_5.
CC DR InterPro; IPR003636; TNF_abc.
CC DR InterPro; IPR000478; TNF_family.
CC DR Pfam; PF00229; TNF; 1.
CC DR ProDom; PD002012; TNF_abc; 1.
CC DR ProDom; PD008600; TNF_5; 1.
CC DR SMART; SM00207; TNF; 1.
CC DR PROSITE; PS00251; TNF_1; 1.
CC DR PROSITE; PS50049; TNF_2; 1.
CC KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
CC FT CHAIN 1 272
CC FT
CC FT CHAIN 111 272
CC FT
CC FT DOMAIN 1 23
CC FT TRANSMEM 24 44
CC FT
CC FT DOMAIN 45 272
CC FT SITE 110 111
CC FT DISULFID 190 229
CC FT CARBOHYD 124 124
CC FT CARBOHYD 146 146
CC FT CARBOHYD 251 251
CC SQ SEQUENCE 272 AA; 30862 MW; 5409F24A8E53CCD7 CRC64;
Query Match 7.9%; Score 103; DB 1; Length 272;
Best Local Similarity 21.6%; Pred. No. 0.064;
Matches 38; Conservative 29; Mismatches 59; Indels 50; Gaps 7;
OY 101 RKRAVLTKQKQKSHLVLPINATSKDDSDVTEVMWQP-----ALRRGRGLQA 150
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 KSRNETSVAERKQPIATHLAGV---KSNTTVRVLKWMTTSYAPTSSLSIYHEGK---- 172
OY 151 QGYGVRIQDAGVYLLYSQVLFQDVTFTMGQVVSREGQGRQETLFR-CIRSMPSHPDR---- 206
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 173 ---LKVEKAGLYIYSQVSF-----CTKAASAPFTLYIYL-YLPMBEDRLMK 217
OY 207 -----AVNSCVSAGVFHLHQGDILSVIIPRARKNLSPHGTFGLGVKL 250
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 218 GLDTHSTALCELOSIREGVPELRQGDWVFVNVTDSTA-VVNVNPGNTYFGMFKL 272
RESULT 13
TNFA_RABIT
ID TNFA_RABIT STANDARD; PRT; 235 AA.
AC P04924;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha)--(Tumor necrosis factor
  ligand superfamily member 2) (Cachectin).
  TNF OR TNFSF2 OR TNFA.
  OS Oryctolagus cuniculus (Rabbit).
  OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
  OC NCBI_TaxID=9986;
  OX NCBI_TaxID=9986;
  RN [1]
  RP SEQUENCE FROM N.A.
  RX MEDLINE=91065534; PubMed=2249779;
  RA Shakhov A.N., Kupraash D.V., Azizov M.M., Jongeneel C.V.,
  RA Nedospasov S.A.;
  RT "Structural analysis of the rabbit TNF locus, containing the genes
  RT encoding TNF-beta (lymphotoxin) and TNF-alpha (tumor necrosis
  RT factor)".;
  RT Gene 95:215-221(1990).
  RN [2]
  RP SEQUENCE FROM N.A.
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RX MEDLINE=86219712; PubMed=3519138;
RA Ito H., Shirai T., Yamamoto S., Akira M., Kawahara S., Todd C.W.,
RA Wallace R.B.;
RT "Molecular cloning of the gene encoding rabbit tumor necrosis
RT factor.";
RL DNA 5:157-165 (1986).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=86219711; PubMed=3519137;
RA Ito H., Yamamoto S., Kuroda S., Sakamoto H., Kajihara J., Kiyota T.,
RA Hayashi H., Kato M., Seko M.;
RT "Molecular cloning and expression in Escherichia coli of the cDNA
RT coding for rabbit tumor necrosis factor.";
RL DNA 5:149-156 (1986).
CC -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
CC induce cell death of certain tumor cell lines. It is potent
CC pyrogen causing fever by direct action or by stimulation of
CC interleukin 1 secretion and is implicated in the induction of
CC cachexia. Under certain conditions it can stimulate cell
CC proliferation and induce cell differentiation.
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -!- PTM: The membrane form, but not the soluble form, is
CC phosphorylated on serine residues. Dephosphorylation of the
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC similarity).
CC -!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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CC -----
DR EMBL; M12845; AAA31486.1; -.
DR EMBL; M12846; AAA31482.1; -.
DR EMBL; M60340; AAA31484.1; -.
DR PIR; A25451; A25451.
DR PIR; A25454; A25454.
DR PIR; J50727; J50727.
DR HSSP; P06804; 2TNF.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR PRODom; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KW Cytokine; Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor.
FT CHAIN 1 235
FT CHAIN 80 235
FT DOMAIN 1 35
FT TRANSMEM 36 56
FT DOMAIN 57 235
FT SITE 79 80
FT MOD_RES 2 2
FT DISULFID 148 179
FT CONFLICT 63 63
SQ SEQUENCE 235 AA; 25816 MW; 610177D0BD2EF871 CRC64;
Query Match 7.9%; Score 102.5; DB 1; Length 235;
Best Local Similarity 24.6%; Pred. No. 0.059;

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Matches 49; Conservative 28; Mismatches 53; Indels 69; Gaps 12;
QY 104 RAVLTQKQKHSHVHL-----VPINATSK--DSDVTEVMWQPAL-----RRGR 146
| : : : : | | : : : : | : : : : | : : : : |
Db 54 RVIGPQEEEGSPNNLHLVNPVAQMTLRSASRALSDKPLAHVYANPOVEGQLWLSQRAN 113
| : : : : | | : : : : | : : : : | : : : : |
QY 147 GLQAQGYGVRIOD-----AGVLLYSQVLFQDVTFTMGQVVSREGQG----- 188
| : : : : | | : : : : | : : : : | : : : : |
Db 114 ALLAN--GMKLTDLNQLVVPADGLYLISQVLF-----SGQGRSVLLTHTV 158
| : : : : | | : : : : | : : : : | : : : : |
QY 189 -----RQETLFRGIRSMDSH---PDRA-----YNSCYAGVFHLHGGDILSVIIPRA 232
| : : : : | | : : : : | : : : : | : : : : |
Db 159 SRFAVSYPNKVNLLSAISK--PCHRETPBEAEPMAYEPIYLGVFQLEKGRDLSDEVNQ 217
| : : : : | | : : : : | : : : : | : : : : |
QY 233 RAKNLSPHG-TFLGFVKL 250
| : : : : | | : : : : | : : : : | : : : : |
Db 218 E-YLDLAESGQVYFGIIL 235
| : : : : | | : : : : | : : : : | : : : : |
RESULT 14
TNF6_MACMU STANDARD; PRT; 280 AA.
AC Q9MYL6; Q9BDM5;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
DE (CD95L protein).
GN TNFSF6 OR FASL OR CD95L.
OS Macaca mulatta (Rhesus macaque),
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
OS Macaca nemestrina (Pig-tailed macaque).
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544, 9541, 9545;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta; TISSUE=Lymphocytes;
RX MEDLINE=21383618; PubMed=11491535;
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta, M.fascicularis, and M.nemestrina;
RA Kirii Y., Inoue T., Yoshino K.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
CC transduces the apoptotic signal into cells. May be involved in
CC cytotoxic T cell mediated apoptosis and in T cell development.
CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
CC peripheral tolerance, in the antigen-stimulated suicide of mature
CC T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3
CC modulates its effects (By similarity).
CC -!- SUBUNIT: Homotrimer (Potential).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
CC similarity).
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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CC -----
DR EMBL; AF344856; AAK37539.1; -.

```

DR EMBL; AB035138; BAA90294.1; -
DR EMBL; AB035139; BAA90295.1; -
DR EMBL; AB035140; BAA90296.1; -
DR HSSP; P01375; 4TSV.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PRO1234; TNECROSISFCT.
DR ProDom; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KW Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.
FT CHAIN 1 280 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT CHAIN 1 280 MEMBER 6, MEMBRANE FORM.
FT CHAIN 129 280 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT DOMAIN 1 80 MEMBER 6, SOLUBLE FORM (BY SIMILARITY).
FT TRANSMEM 81 101 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
DOMAIN 102 280 EXTRACELLULAR (POTENTIAL).
DOMAIN 4 69 PRO-RICH.
FT SITE 128 129 CLEAVAGE (BY SIMILARITY).
FT DISULFID 201 232 POTENTIAL.
FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 249 249 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 60 60 S -> P (IN REF. 1).
SQ SEQUENCE 280 AA; 31367 MW; FOH284D61A132EB4 CRC64;

Query Match 7.9%; Score 102.5; DB 1; Length 280;
Best Local Similarity 22.3%; Pred. No. 0.074;
Matches 61; Conservative 32; Mismatches 107; Indels 73; Gaps 9;

QY 2 PASSPFLAPKGPNGGPPVREPALVALWLSGALGAVACAMALITQOTELQSLRE 61
DB 57 PPPSPPLPLPLPKKRGHSTGLCLVFMVLVALVGLGMFQLHQLKELALRES 116
QY 62 VSRLQGTGSPQNGEGYFWSLPQSSDALAEWNGERSRKRRAVLTKQKQKSHVHLV 121
DB 117 TSQ-KHTASSLEKQIGHP--SPPE-----KKEQRKVAHL- 148
QY 122 PINATSKDSDVTEVMWQP--ALRRGRGLQAQGYGVRIDAGVYLYSOVLF----- 171
DB 149 ---TGKPNRSRSMPLWEDTYGIVLLSGVKYKKGGLVINETGLYFVYSKYVFRGQSTNL 204
QY 172 -----QDVTFTMGQVVSREGGROETLFRICRSMPSHPDRAYNSCYSAGVF 217
DB 205 PLSHKYVMRSKYPPQDLVMEGKMSYCTTGQ-----MMAH-----SSYLGAVF 248
QY 218 HLHGDIISVITPRARAKNLSPHGTFGLFVKL 250
DB 249 NLTSADHLVNVSEL-SLVNFEESQTFGLYKL 280

RESULT 15
TNFA_CEREL STANDARD; PRT; 229 AA.
AC P51743;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
ligand superfamily member 2) (Cachectin) (Fragment).
GN TNF OR TNFSF2 OR TNFA.
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.

RA Lockhart E.A.;
CC Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
CC induce cell death of certain tumor cell lines. It is potent
CC pyrogen causing fever by direct action or by stimulation of
CC interleukin 1 secretion and is implicated in the induction of
CC cachexia, under certain conditions it can stimulate cell
CC proliferation and induce cell differentiation.
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
CC -!- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC PROTEOLYTIC PROCESSING (BY SIMILARITY).
CC -!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; U14683; AAA50759.1; -
DR HSSP; P01375; 4TSV.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KW Cytokine; Cytotoxin; Transmembrane; Signal-anchor.
FT NON TER 1 1
FT CHAIN <1 229 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
FT CHAIN 74 229 TUMOR NECROSIS FACTOR, SOLUBLE FORM.
FT DOMAIN <1 30 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 31 51 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 52 229 EXTRACELLULAR (POTENTIAL).
FT SITE 72 73 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
FT DISULFID 141 173 BY SIMILARITY.
SQ SEQUENCE 229 AA; 24987 MW; 16DE5F7AA5A7DB35 CRC64;

Query Match 7.7%; Score 100; DB 1; Length 229;
Best Local Similarity 29.4%; Pred. No. 0.095;
Matches 48; Conservative 24; Mismatches 39; Indels 52; Gaps 13;

QY 106 VLTQKQKQHS---VLHLVP-INATSKDSDVTEVMWQPALRRGRGLQAQGYGVRID- 159
DB 70 VQTLRSSQASINKPAHVAVANINAQG-----QLMLDSC--ANALMAN--GVKLEDN 118
QY 160 -----AGVYLYSOVLFD-----VTFTMGQV-VSREGGROETLFRICRSMPSH 203
DB 119 QLVVPTDGLYLYISOVLFRGQSCSTPLFLTHITSRIAVSYQ---TKVNITSAIKS-PCH 174
QY 204 ---PDRA-----YNSCYSAGVFHLHGQDILSVITPRARAKNL 238
DB 175 RETPEWAEMAKPWEPPIYQGGVFQLEKGDRLS-----AEINL 210

Search completed: March 26, 2003, 07:31:58
Job time : 12 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 07:45:50 ; Search time 28 Seconds
(without alignments)
262.705 Million cell updates/sec

Title: US-09-724-341-8
Perfect score: 250
Sequence: 1 MPASSPFLAPKGPFGNMGC.....RAKAKNLSPHGTFLGFVKL 250

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

d size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database :

- Issued_Patents_AA:*
- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
 - 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
 - 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
 - 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
 - 5: /cgn2_6/ptodata/1/iaa/PCUS_COMB.pep:*
 - 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	250	100.0	250	4 US-08-883-086-2	Sequence 2, Appl1
2	246	98.4	247	4 US-09-157-864-4	Sequence 4, Appl1
3	183	73.2	250	4 US-09-153-927-4	Sequence 4, Appl1
4	162	64.8	205	4 US-09-286-529-5	Sequence 5, Appl1
5	147	58.8	147	4 US-08-883-086-3	Sequence 3, Appl1
6	136	54.4	136	4 US-09-589-287B-20	Sequence 20, Appl1
7	121	48.4	234	4 US-09-157-864-2	Sequence 2, Appl1
8	18	7.2	24	4 US-09-157-864-6	Sequence 6, Appl1
9	10	4.0	16	4 US-09-157-864-8	Sequence 8, Appl1
10	7	2.8	31	4 US-09-181-941-13	Sequence 13, Appl1
11	7	2.8	62	4 US-09-615-192A-300	Sequence 300, Appl1
12	7	2.8	101	3 US-09-034-916-4	Sequence 4, Appl1
13	7	2.8	145	4 US-09-286-529-21	Sequence 21, Appl1
14	7	2.8	155	4 US-09-589-287B-23	Sequence 23, Appl1
15	7	2.8	179	4 US-09-615-192A-299	Sequence 299, Appl1
16	7	2.8	219	4 US-09-589-287B-28	Sequence 28, Appl1
17	7	2.8	219	4 US-09-589-287B-30	Sequence 30, Appl1
18	7	2.8	265	4 US-09-589-287B-19	Sequence 19, Appl1
19	7	2.8	285	4 US-09-286-529-1	Sequence 1, Appl1
20	7	2.8	285	4 US-09-589-287B-2	Sequence 2, Appl1
21	7	2.8	289	4 US-09-589-287B-38	Sequence 38, Appl1
22	7	2.8	336	1 US-08-414-926A-26	Sequence 26, Appl1
23	7	2.8	336	2 US-08-926-922-26	Sequence 26, Appl1
24	7	2.8	336	3 US-09-253-682-26	Sequence 26, Appl1
25	7	2.8	336	4 US-09-527-657-26	Sequence 26, Appl1
26	7	2.8	346	3 US-09-034-916-2	Sequence 2, Appl1
27	7	2.8	364	1 US-08-400-422-3	Sequence 3, Appl1

28	7	2.8	401	4 US-09-462-645C-2	Sequence 2, Appl1
29	7	2.8	401	4 US-09-462-645C-6	Sequence 6, Appl1
30	7	2.8	401	4 US-09-462-645C-10	Sequence 10, Appl1
31	7	2.8	724	4 US-09-562-737-29	Sequence 29, Appl1
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34	7	2.8	1090	5 PCT-US95-11808-3	Sequence 3, Appl1
35	7	2.8	1891	2 US-08-804-227C-12	Sequence 12, Appl1
36	7	2.8	1891	2 US-08-804-198-6	Sequence 6, Appl1
37	7	2.8	2627	2 US-08-751-189-3	Sequence 3, Appl1
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39	7	2.8	2627	4 US-09-184-445-3	Sequence 3, Appl1
40	7	2.8	2629	2 US-08-751-189-4	Sequence 4, Appl1
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43	7	2.8	4150	4 US-09-428-517-2	Sequence 2, Appl1
44	6	2.4	15	1 US-08-107-235-10	Sequence 10, Appl1
45	6	2.4	15	1 US-08-178-268-44	Sequence 44, Appl1
46	6	2.4	15	3 US-08-714-960B-10	Sequence 10, Appl1
47	6	2.4	15	4 US-09-598-784-10	Sequence 10, Appl1
48	6	2.4	15	4 US-09-009-953-142	Sequence 142, App
49	6	2.4	16	4 US-09-157-864-7	Sequence 7, Appl1
50	6	2.4	17	4 US-09-342-681C-119	Sequence 119, App
51	6	2.4	22	4 US-08-690-775-1	Sequence 1, Appl1
52	6	2.4	23	1 US-07-987-286-3	Sequence 3, Appl1
53	6	2.4	23	2 US-08-614-626-3	Sequence 3, Appl1
54	6	2.4	25	1 US-07-987-286-11	Sequence 11, Appl1
55	6	2.4	25	1 US-07-987-286-24	Sequence 24, Appl1
56	6	2.4	25	2 US-08-614-626-11	Sequence 11, Appl1
57	6	2.4	25	2 US-08-614-626-24	Sequence 24, Appl1
58	6	2.4	25	2 US-09-230-548-20	Sequence 20, Appl1
59	6	2.4	30	4 US-09-181-941-9	Sequence 9, Appl1
60	6	2.4	33	4 US-09-181-941-14	Sequence 14, Appl1
61	6	2.4	51	4 US-09-369-494-16	Sequence 16, Appl1
62	6	2.4	51	4 US-09-358-569D-14	Sequence 14, Appl1
63	6	2.4	59	4 US-09-655-270A-30	Sequence 30, Appl1
64	6	2.4	86	4 US-09-247-155-112	Sequence 112, App
65	6	2.4	96	2 US-08-710-749-28	Sequence 28, Appl1
66	6	2.4	106	4 US-08-469-260A-253	Sequence 253, App
67	6	2.4	122	4 US-09-199-637A-353	Sequence 353, App
68	6	2.4	127	4 US-08-858-207A-490	Sequence 490, App
69	6	2.4	129	4 US-09-199-637A-371	Sequence 371, App
70	6	2.4	139	1 US-07-994-469A-10	Sequence 10, Appl1
71	6	2.4	142	2 US-08-997-080-47	Sequence 47, Appl1
72	6	2.4	142	2 US-08-997-362-47	Sequence 47, Appl1
73	6	2.4	142	3 US-08-873-970-47	Sequence 47, Appl1
74	6	2.4	142	4 US-09-095-855-47	Sequence 47, Appl1
75	6	2.4	142	4 US-08-705-347A-47	Sequence 47, Appl1
76	6	2.4	142	4 US-09-324-542-47	Sequence 47, Appl1
77	6	2.4	142	4 US-09-205-426-47	Sequence 47, Appl1
78	6	2.4	142	4 US-09-200-643-47	Sequence 47, Appl1
79	6	2.4	145	1 US-07-994-469A-9	Sequence 9, Appl1
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81	6	2.4	147	4 US-09-105-343A-9	Sequence 9, Appl1
82	6	2.4	148	1 US-07-668-517-2	Sequence 2, Appl1
83	6	2.4	148	1 US-07-668-517-15	Sequence 15, Appl1
84	6	2.4	148	4 US-09-724-864-41	Sequence 41, Appl1
85	6	2.4	149	1 US-07-668-517-3	Sequence 3, Appl1
86	6	2.4	149	1 US-07-668-517-16	Sequence 16, Appl1
87	6	2.4	150	1 US-07-668-517-4	Sequence 4, Appl1
88	6	2.4	150	1 US-07-668-517-5	Sequence 5, Appl1
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91	6	2.4	150	1 US-07-668-517-9	Sequence 9, Appl1
92	6	2.4	150	1 US-07-668-517-10	Sequence 10, Appl1
93	6	2.4	150	1 US-07-668-517-11	Sequence 11, Appl1
94	6	2.4	150	1 US-07-668-517-12	Sequence 12, Appl1
95	6	2.4	150	1 US-07-668-517-13	Sequence 13, Appl1
96	6	2.4	150	1 US-07-668-517-14	Sequence 14, Appl1
97	6	2.4	150	1 US-07-668-517-17	Sequence 17, Appl1
98	6	2.4	150	1 US-07-668-517-29	Sequence 29, Appl1
99	6	2.4	150	1 US-07-668-517-31	Sequence 31, Appl1
100	6	2.4	150	1 US-07-668-517-35	Sequence 35, Appl1

ALIGNMENTS

RESULT 1

US-08-883-086-2
; Sequence 2, Application US/08883086
; Patent No. 6171787
; GENERAL INFORMATION:
; APPLICANT: WILEY, STEVEN
; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
; TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/883,086
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Potembski, Priscilla E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 6134.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-937-0378
; TELEFAX: 847-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 250 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6171787e
; -08-883-086-2

Query Match 100.0%; Score 250; DB 4; Length 250;
Best Local Similarity 100.0%; Pred. No. 1e-231;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPASSPFLAPKGPNGMGVREPALSVLWLSWGALGAVACAMALLTQOTELQSLRR 60
Db 1 MPASSPFLAPKGPNGMGVREPALSVLWLSWGALGAVACAMALLTQOTELQSLRR 60
QY 61 EVSRLQGTGSPSQNGEGYPWQSLPEQSSDALAEWENGERSRKRRAVLTKQKKQHSVLHL 120
Db 61 EVSRLQGTGSPSQNGEGYPWQSLPEQSSDALAEWENGERSRKRRAVLTKQKKQHSVLHL 120
QY 121 VPINATSKDSDVTEVMWQPALRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQ 180
Db 121 VPINATSKDSDVTEVMWQPALRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQ 180
QY 181 VVSREGQGRQETLFRICIRSMPSHPDRAYNSCYSGVFHLHOGDILSVIIPRARA KLNLSLSP 240
Db 181 VVSREGQGRQETLFRICIRSMPSHPDRAYNSCYSGVFHLHOGDILSVIIPRARA KLNLSLSP 240
QY 241 HGTFLGFVKL 250
Db 241 HGTFLGFVKL 250

RESULT 2

US-09-157-864-4
; Sequence 4, Application US/09157864
; Patent No. 6440694
; GENERAL INFORMATION:
; APPLICANT: Bienkowski, Michael J
; APPLICANT: Mills, Cynthia J
; APPLICANT: Jones, David A
; TITLE OF INVENTION: TNF-Related Death Ligand
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Pharmacia & Upjohn, Intellectual Property
; STREET: 301 Henrietta Street
; CITY: Kalamazoo
; STATE: MI
; COUNTRY: USA
; ZIP: 49001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/157,864
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerber, Lori L.
; REGISTRATION NUMBER: 41,113
; REFERENCE/DOCKET NUMBER: 6111.N CNI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 616/833-0974
; TELEFAX: 616/833-8897
; TELEX: 224401
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-157-864-4

Query Match 98.4%; Score 246; DB 4; Length 247;
Best Local Similarity 100.0%; Pred. No. 6.7e-228;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 EVSRLQGTGSPSQNGEGYPWQSLPEQSSDALAEWENGERSRKRRAVLTKQKKQHSVLHL 120
Db 61 EVSRLQGTGSPSQNGEGYPWQSLPEQSSDALAEWENGERSRKRRAVLTKQKKQHSVLHL 120
QY 121 VPINATSKDSDVTEVMWQPALRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQ 180
Db 121 VPINATSKDSDVTEVMWQPALRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQ 180
QY 181 VVSREGQGRQETLFRICIRSMPSHPDRAYNSCYSGVFHLHOGDILSVIIPRARA KLNLSLSP 240
Db 181 VVSREGQGRQETLFRICIRSMPSHPDRAYNSCYSGVFHLHOGDILSVIIPRARA KLNLSLSP 240
QY 241 HGTFLG 246
Db 241 HGTFLG 246

RESULT 3
US-09-153-927-4

;; TITLE OF INVENTION: Antibodies to Neutrokin-alpha
;; FILE REFERENCE: PF343P3C1
;; CURRENT APPLICATION NUMBER: US/09/589,287B
;; CURRENT FILING DATE: 2000-06-08
;; Prior application data removed - check PALM or file wrapper
;; NUMBER OF SEQ ID NOS: 42
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 20
;; LENGTH: 136
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-589-287B-20

Query Match 54.4%; Score 136; DB 4; Length 136;
Best Local Similarity 100.0%; Pred. No. 9e-123;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 HSVLHLPINATSKDSDVTEVMQPALRRGRLQAQGYGVRIQDAGVYLLYSQVLFQDV 174
1 HSVLHLPINATSKDSDVTEVMQPALRRGRLQAQGYGVRIQDAGVYLLYSQVLFQDV 60
175 TFTMGQVVSREGQGRQETLFCIRSMSPHDPDRAYNSCYSAGVFHLHQGDILSVIIPARA 234
Db 61 TFTMGQVVSREGQGRQETLFCIRSMSPHDPDRAYNSCYSAGVFHLHQGDILSVIIPARA 120
QY 235 KNLSPHGTFLGFKL 250
Db 121 KNLSPHGTFLGFKL 136

RESULT 7

US-09-157-864-2

; Sequence 2, Application US/09157864

; Patent No. 6440694

; GENERAL INFORMATION:

; APPLICANT: Bienkowski, Michael J

; APPLICANT: Mills, Cynthia J

; APPLICANT: Jones, David A

; TITLE OF INVENTION: TNF-Related Death Ligand

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pharmacia & Upjohn, Intellectual Property

; ADDRESSEE: Legal Services

; STREET: 301 Henrietta Street

; CITY: Kalamazoo

; STATE: MI

; COUNTRY: USA

; ZIP: 49001

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 Diskette

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/157,864

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Kerber, Lori L.

; REGISTRATION NUMBER: 41,113

; REFERENCE/DOCKET NUMBER: 6111.N CN1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 616/833-0974

; TELEFAX: 616/833-8897

; TELEX: 224401

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 234 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-09-157-864-2

Query Match 48.4%; Score 121; DB 4; Length 234;
Best Local Similarity 100.0%; Pred. No. 3.4e-108;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 DSDVTEVMQPALRRGRLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQVVSREGQGR 189
Db 114 DSDVTEVMQPALRRGRLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQVVSREGQGR 173
QY 190 QETLFCIRSMSPHDPDRAYNSCYSAGVFHLHQGDILSVIIPARAKNLSPHGTFLGFK 249
Db 174 QETLFCIRSMSPHDPDRAYNSCYSAGVFHLHQGDILSVIIPARAKNLSPHGTFLGFK 233

QY 250 L 250
Db 234 L 234

RESULT 8

US-09-157-864-6

; Sequence 6, Application US/09157864

; Patent No. 6440694

; GENERAL INFORMATION:

; APPLICANT: Bienkowski, Michael J

; APPLICANT: Mills, Cynthia J

; APPLICANT: Jones, David A

; TITLE OF INVENTION: TNF-Related Death Ligand

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pharmacia & Upjohn, Intellectual Property

; ADDRESSEE: Legal Services

; STREET: 301 Henrietta Street

; CITY: Kalamazoo

; STATE: MI

; COUNTRY: USA

; ZIP: 49001

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 Diskette

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/157,864

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Kerber, Lori L.

; REGISTRATION NUMBER: 41,113

; REFERENCE/DOCKET NUMBER: 6111.N CN1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 616/833-0974

; TELEFAX: 616/833-8897

; TELEX: 224401

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 24 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-09-157-864-6

Query Match 7.2%; Score 18; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 AGVFHLHQGDILSVIIPR 231
Db 7 AGVFHLHQGDILSVIIPR 24

RESULT 9

US-09-157-864-8


```
/ Sequence 8, Application US/09157864
/ Patent No. 6440694
/ GENERAL INFORMATION:
/ APPLICANT: Bienkowski, Michael J
/ APPLICANT: Mills, Cynthia J
/ APPLICANT: Jones, David A
/ TITLE OF INVENTION: TNF-Related Death Ligand
/ NUMBER OF SEQUENCES: 18
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pharmacia & Upjohn, Intellectual Property
/ ADDRESSEE: Legal Services
/ STREET: 301 Henrietta Street
/ CITY: Kalamazoo
/ STATE: MI
/ COUNTRY: USA
/ ZIP: 49001
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 Diskette
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/157,864
/ FILING DATE:
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Kerber, Lori L.
/ REGISTRATION NUMBER: 41,113
/ REFERENCE/DOCKET NUMBER: 6111.N CN1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 616/833-0974
/ TELEFAX: 616/833-8897
/ TELEX: 224401
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 16 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-09-157-864-8

Query Match          4.0%; Score 10; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 157 IQDAGVYLLY 166
  |||||||
  1 IQDAGVYLLY 10

RESULT 10
US-09-181-941-13
/ Sequence 13, Application US/09181941
/ Patent No. 6440690
/ GENERAL INFORMATION:
/ APPLICANT: Mor, Amram
/ APPLICANT: Vouldoukis, Ioannis
/ APPLICANT: Nicolaie, Pierre
/ TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION
/ OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS
/ NUMBER OF SEQUENCES: 16
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds LLP
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: NY
/ COUNTRY: USA
/ ZIP: 10036-2811
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: Windows
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/ SOFTWARE: FastSEQ for Windows Version 2.0b
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/181,941
/ FILING DATE: 28-Oct-1998
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/574,701
/ FILING DATE: 19-DEC-1995
/ APPLICATION NUMBER: FR 95 07831
/ FILING DATE: 29-JUN-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 3909-0021-999
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-493-4935
/ TELEFAX: 650-493-5556
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 13:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 31 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: NO. 6440690E
/ SEQUENCE DESCRIPTION: SEQ ID NO: 13:
/ US-09-181-941-13

Query Match          2.8%; Score 7; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 37 AALGAVA 43
  |||||||
Db 20 AALGAVA 26
```

```
RESULT 11
US-09-615-192A-300
/ Sequence 300, Application US/09615192A
/ Patent No. 6410718
/ GENERAL INFORMATION:
/ APPLICANT: Bloksberg, Leonard N.
/ APPLICANT: Havukkala, Ilkka
/ TITLE OF INVENTION: Materials and Methods for the
/ MODIFICATION OF PLANT LIGNIN CONTENT
/ FILE REFERENCE: 11000.1003C4U
/ CURRENT APPLICATION NUMBER: US/09/615,192A
/ CURRENT FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 08/975,316
/ PRIOR FILING DATE: 1997-11-21
/ PRIOR APPLICATION NUMBER: US 08/713,000
/ PRIOR FILING DATE: 1996-09-11
/ PRIOR APPLICATION NUMBER: US 09/169,789
/ PRIOR FILING DATE: 1998-10-09
/ NUMBER OF SEQ ID NOS: 405
/ SOFTWARE: FastSEQ for Windows Version 3.0
/ SEQ ID NO 300
/ LENGTH: 62
/ TYPE: PRT
/ ORGANISM: Eucalyptus grandis
/ US-09-615-192A-300
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```
Query Match          2.8%; Score 7; DB 4; Length 62;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 242 GTPLGFV 248
  |||||||
Db 5 GTPLGFV 11
```

RESULT 12

US-09-034-916-4
; Sequence 4, Application US/09034916
; Patent No. 6046314
; GENERAL INFORMATION:
; APPLICANT: GEBE, JOHN A.
; APPLICANT: SIADAK, ANTHONY W.
; APPLICANT: ARUFFO, ALEJANDRO A.
; TITLE OF INVENTION: SPALPHA: A NOVEL SCAVENGER RECEPTOR
; TITLE OF INVENTION: CYSTEINE-RICH DOMAIN-CONTAINING POLYPEPTIDE AND MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES THERETO
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBINS & ASSOCIATES
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/034,916
; FILING DATE: 04-MAR-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/039,956
; FILING DATE: 06-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINS, ROBERTA L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 5998-0020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 325-7812
; TELEFAX: (650) 325-7823
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 101 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-034-916-4
Query Match 2.8%; Score 7; DB 3; Length 101;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 104 RAVLTQK 110
Db 45 RAVLTQK 51
RESULT 13
US-09-286-529-21
; Sequence 21, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/286,529
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-286-529-21

Query Match 2.8%; Score 7; DB 4; Length 145;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 209 NSCYSAG 215
Db 103 NSCYSAG 109
RESULT 14
US-09-589-287B-23
; Sequence 23, Application US/09589287B
; Patent No. 6403770
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Antibodies to Neutrokin-alpha
; FILE REFERENCE: PF343P3C1
; CURRENT APPLICATION NUMBER: US/09/589,287B
; CURRENT FILING DATE: 2000-06-08
; Prior application data removed - check PALM or file wrapper
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 23
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-589-287B-23

Query Match 2.8%; Score 7; DB 4; Length 155;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 209 NSCYSAG 215
Db 113 NSCYSAG 119

RESULT 15
US-09-615-192A-299
; Sequence 299, Application US/09615192A
; Patent No. 6410718
; GENERAL INFORMATION:
; APPLICANT: Bloksberg, Leonard N.
; APPLICANT: Havukkala, Ilkka
; TITLE OF INVENTION: Materials and Methods for the
; TITLE OF INVENTION: Modification of Plant Lignin Content
; FILE REFERENCE: 11000.1003c4U
; CURRENT APPLICATION NUMBER: US/09/615,192A
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 08/975,316
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 08/713,000
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: US 09/169,789
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 299
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-09-615-192A-299

Query Match 2.8%; Score 7; DB 4; Length 179;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 242 GTFLGFV 248
Db 16 GTFLGFV 22

RESULT 16

```
US-09-589-287B-28
; Sequence 28, Application US/09589287B
; Patent No. 6403770
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Antibodies to Neutrokin-alpha
; FILE REFERENCE: PF343P3C1
; CURRENT APPLICATION NUMBER: US/09/589,287B
; CURRENT FILING DATE: 2000-06-08
; Prior application data removed - check PALM or file wrapper
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-589-287B-28

Query Match
Best Local Similarity 2.8%; Score 7; DB 4; Length 219;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 NSCYSAG 215
|||
Db 177 NSCYSAG 183

RESULT 17
US-09-589-287B-30
; Sequence 30, Application US/09589287B
; Patent No. 6403770
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Antibodies to Neutrokin-alpha
; FILE REFERENCE: PF343P3C1
; CURRENT APPLICATION NUMBER: US/09/589,287B
; CURRENT FILING DATE: 2000-06-08
; Prior application data removed - check PALM or file wrapper
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-589-287B-30

Query Match
Best Local Similarity 2.8%; Score 7; DB 4; Length 219;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 NSCYSAG 215
|||
Db 177 NSCYSAG 183

RESULT 18
US-09-589-287B-19
; Sequence 19, Application US/09589287B
; Patent No. 6403770
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Antibodies to Neutrokin-alpha
; FILE REFERENCE: PF343P3C1
; CURRENT APPLICATION NUMBER: US/09/589,287B
; CURRENT FILING DATE: 2000-06-08
; Prior application data removed - check PALM or file wrapper
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-589-287B-19
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```
Query Match
Best Local Similarity 2.8%; Score 7; DB 4; Length 266;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 NSCYSAG 215
|||
Db 224 NSCYSAG 230

RESULT 19
US-09-286-529-1
; Sequence 1, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/286,529
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 285
; TYPE: PRT
; ORGANISM: human
US-09-286-529-1

Query Match
Best Local Similarity 2.8%; Score 7; DB 4; Length 285;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 NSCYSAG 215
|||
Db 243 NSCYSAG 249

RESULT 20
US-09-589-287B-2
; Sequence 2, Application US/09589287B
; Patent No. 6403770
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Antibodies to Neutrokin-alpha
; FILE REFERENCE: PF343P3C1
; CURRENT APPLICATION NUMBER: US/09/589,287B
; CURRENT FILING DATE: 2000-06-08
; Prior application data removed - check PALM or file wrapper
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 285
; TYPE: PRT
; ORGANISM: human
US-09-589-287B-2

Query Match
Best Local Similarity 2.8%; Score 7; DB 4; Length 285;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 NSCYSAG 215
|||
Db 243 NSCYSAG 249

RESULT 21
US-09-589-287B-38
; Sequence 38, Application US/09589287B
; Patent No. 6403770
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Antibodies to Neutrokin-alpha
; FILE REFERENCE: PF343P3C1
```

; CURRENT APPLICATION NUMBER: US/09/589,287B
; CURRENT FILING DATE: 2000-06-08
; Prior application data removed - check PALM or file wrapper
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-589-287B-38

Query Match 2.8%; Score 7; DB 4; Length 289;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 209 NSCYSAG 215
|||
Db 247 NSCYSAG 253

SULT 22
-08-414-926A-26
; Sequence 26, Application US/08414926A
; Patent No. 5721354
; GENERAL INFORMATION:
; APPLICANT: Spaete, Richard
; TITLE OF INVENTION: NOVEL HUMAN CYTOMEGALOVIRUS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,926A
; FILING DATE: March 31, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Cseert, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: AVIR-011/OOUS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-494-7622
; TELEFAX: 415-857-0663
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: col.22
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..336
; OTHER INFORMATION: /label= UL151
US-08-414-926A-26

Query Match 2.8%; Score 7; DB 1; Length 336;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 142 LRRGRL 148
|||
Db 82 LRRGRL 88

RESULT 23
US-08-926-922-26

; Sequence 26, Application US/08926922
; Patent No. 5925751
; GENERAL INFORMATION:
; APPLICANT: Spaete, Richard
; APPLICANT: Cha, Tai-An
; TITLE OF INVENTION: NOVEL HUMAN CYTOMEGALOVIRUS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Luann Cseert Attorney at Law
; STREET: 750 Arimo Avenue
; CITY: Oakland
; STATE: CA
; COUNTRY: USA
; ZIP: 94610

COMPUTER READABLE FORM:

; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,922
; FILING DATE: September 10, 1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Cseert, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: AVIR 11A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-834-1448
; TELEFAX: 510-839-7810

; INFORMATION FOR SEQ ID NO: 26:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: col.22
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..336
; OTHER INFORMATION: /label= UL151

US-08-926-922-26

Query Match 2.8%; Score 7; DB 2; Length 336;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 142 LRRGRL 148
|||
Db 82 LRRGRL 88

RESULT 24

US-09-253-682-26

; Sequence 26, Application US/09253682
; Patent No. 6040170
; GENERAL INFORMATION:
; APPLICANT: Spaete, Richard
; APPLICANT: Cha, Tai-An
; TITLE OF INVENTION: NOVEL HUMAN CYTOMEGALOVIRUS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Luann Cseert Attorney at Law
; STREET: 750 Arimo Avenue
; CITY: Oakland
; STATE: CA
; COUNTRY: USA
; ZIP: 94610

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/253,682
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/926,922
; FILING DATE: September 10, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: AVIR 11A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-834-1448
; TELEFAX: 510-839-7810
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: col.22
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..336
; OTHER INFORMATION: /label= UL151
;
US-09-253-682-26

Query Match      2.8%; Score 7; DB 3; Length 336;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 142 LRRGRGL 148
Db 82 LRRGRGL 88

RESULT 25
US-09-527-657-26
; Sequence 26, Application US/09527657
; Patent No. 6291236
; GENERAL INFORMATION:
; APPLICANT: Spaete, Richard
; Cha, Tai-An
; TITLE OF INVENTION: NOVEL HUMAN CYTOMEGALOVIRUS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Luann Cserr Attorney at Law
; STREET: 750 Arimo Avenue
; CITY: Oakland
; STATE: CA
; COUNTRY: USA
; ZIP: 94610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/527,657
; FILING DATE: 17-Mar-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,922
; FILING DATE: September 10, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserr, Luann
; REGISTRATION NUMBER: 31,822
```

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; REFERENCE/DOCKET NUMBER: AVIR 11A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-834-1448
; TELEFAX: 510-839-7810
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: col.22
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..336
; OTHER INFORMATION: /label= UL151
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
;
US-09-527-657-26

Query Match      2.8%; Score 7; DB 4; Length 336;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 142 LRRGRGL 148
Db 82 LRRGRGL 88

RESULT 26
US-09-034-916-2
; Sequence 2, Application US/09034916
; Patent No. 6046314
; GENERAL INFORMATION:
; APPLICANT: GEBE, JOHN A.
; APPLICANT: SIADAK, ANTHONY W.
; APPLICANT: ARUFFO, ALEJANDRO A.
; TITLE OF INVENTION: SPALPHA: A NOVEL SCAVENGER RECEPTOR
; TITLE OF INVENTION: CYSTEINE-RICH DOMAIN-CONTAINING POLYPEPTIDE AND MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES THEREFO
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBINS & ASSOCIATES
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/034,916
; FILING DATE: 04-MAR-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/039,956
; FILING DATE: 06-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINS, ROBERTA L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 5998-0020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 325-7812
; TELEFAX: (650) 325-7823
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 346 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-09-034-916-2
```

Query Match 2.8%; Score 7; DB 3; Length 346;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 104 RAVLTOK 110
Db 182 RAVLTOK 188

RESULT 27

US-08-400-422-3
; Sequence 3, Application US/08400422
; Patent No. 5681715
; GENERAL INFORMATION:
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Diderichsen, Boerge Krag
; APPLICANT: Buckley, Catherine M.
; APPLICANT: Hobson, Audrey
; APPLICANT: McConnell, David J.
; TITLE OF INVENTION: A process for the preparation of an active
; TITLE OF INVENTION: lipase
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 56817150 No. 5681715disk of No. 5681715th America, Inc.
; STREET: 405 Lexington Avenue, 62nd floor
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/400,422
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/038,763
; FILING DATE: 25-MAR-1993
; APPLICATION NUMBER: PCT/DK91/00402
; FILING DATE: 20-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK92/00391
; FILING DATE: 18-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 3663,200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 364 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Pseudomonas cepacia
; STRAIN: DSM 3401
; US-08-400-422-3

Query Match 2.8%; Score 7; DB 1; Length 364;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 40 GAVACAM 46
Db 12 GAVACAM 18

RESULT 28

US-09-462-645C-2
; Sequence 2, Application US/09462645C
; Patent No. 6436681
; GENERAL INFORMATION:
; APPLICANT: Schroeder, Hartwig
; APPLICANT: Hauer, Bernhard
; TITLE OF INVENTION: The preparation of biotin
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/462,645C
; CURRENT FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: PCT/EP98/04097
; PRIOR FILING DATE: 1998-02-07
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: WordPerfect version 6.1
; SEQ ID NO 2
; LENGTH: 401
; TYPE: PRT
; ORGANISM: E. Coli w3110
; US-09-462-645C-2

Query Match 2.8%; Score 7; DB 4; Length 401;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 158 QDAGVYL 164
Db 17 QDAGVYL 23

RESULT 29

US-09-462-645C-6
; Sequence 6, Application US/09462645C
; Patent No. 6436681
; GENERAL INFORMATION:
; APPLICANT: Schroeder, Hartwig
; APPLICANT: Hauer, Bernhard
; TITLE OF INVENTION: The preparation of biotin
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/462,645C
; CURRENT FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: PCT/EP98/04097
; PRIOR FILING DATE: 1998-02-07
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: WordPerfect version 6.1
; SEQ ID NO 6
; LENGTH: 401
; TYPE: PRT
; ORGANISM: clone pHS1bios1
; US-09-462-645C-6

Query Match 2.8%; Score 7; DB 4; Length 401;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 158 QDAGVYL 164
Db 17 QDAGVYL 23

RESULT 30

US-09-462-645C-10
; Sequence 10, Application US/09462645C
; Patent No. 6436681
; GENERAL INFORMATION:
; APPLICANT: Schroeder, Hartwig
; APPLICANT: Hauer, Bernhard
; TITLE OF INVENTION: The preparation of biotin

FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/462,645C
CURRENT FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: PCT/EP98/04097
PRIOR FILING DATE: 1998-02-07
NUMBER OF SEQ ID NOS: 38
SOFTWARE: wordPerfect version 6.1
SEQ ID NO 10
LENGTH: 401
TYPE: PRT
ORGANISM: clone PHS2bioS1
US-09-462-645C-10

Query Match
Best Local Similarity 100.0%; Pred. No. 87;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 158 QDAGVYL 164
|||
Db 17 QDAGVYL 23

RESULT 31
US-09-562-737-29
Sequence 29, Application US/09562737
Patent No. 6428967
GENERAL INFORMATION:
APPLICANT: Herz, Joachim
APPLICANT: Gotthardt, Michael
TITLE OF INVENTION: LDL Receptor Signaling Pathways
FILE REFERENCE: UTSW0708
CURRENT APPLICATION NUMBER: US/09/562,737
CURRENT FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 132
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 29
LENGTH: 724
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-562-737-29

Query Match
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

59 RREVSRL 65
|||
Db 496 RREVSRL 502

RESULT 32
US-08-307-896-3
Sequence 3, Application US/08307896C
Patent No. 6034071
GENERAL INFORMATION:
APPLICANT: Iyengar, Srinivas Ravi
TITLE OF INVENTION: MUTANT ACTIVATED GSALPHA AND ADENYLYL
TITLE OF INVENTION: CYCLASE 2 FOR USE AS THERAPEUTIC AGENTS
FILE REFERENCE: 29770
CURRENT APPLICATION NUMBER: US/08/307,896C
CURRENT FILING DATE: 1994-09-16
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 1090
TYPE: PRT
ORGANISM: Rattus norvegicus
US-08-307-896-3

Query Match 2.8%; Score 7; DB 3; Length 1090;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 166 YSQVLFQ 172
|||
Db 787 YSQVLFQ 793

RESULT 33
US-08-726-214-4
Sequence 4, Application US/08726214
Patent No. 6107076
GENERAL INFORMATION:
APPLICANT: Tang, Wei-Jen
APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,214
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,498
FILING DATE: 04-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UTS0:450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1090 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-726-214-4

Query Match
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 166 YSQVLFQ 172
|||
Db 787 YSQVLFQ 793

RESULT 34
PCT-US95-11808-3
Sequence 3, Application PC/TUS9511808
GENERAL INFORMATION:
APPLICANT: Iyengar, Srinivas Ravi V.
TITLE OF INVENTION: MUTANT ACTIVATED GSALPHA AND
TITLE OF INVENTION: ADENYLYL
TITLE OF INVENTION: CYCLASE 2 FOR USE AS THERAPEUTIC AGENTS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brumbaugh, Graves, Donohue and
ADDRESS: Raymond

STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.
ZIP: 10112-0228
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11808
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/307,896
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Richard S.
REGISTRATION NUMBER: 26,154
REFERENCE/DOCKET NUMBER: 29970 165/28755
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 408-2500
TELEFAX: (212) 765-2519
TELEX: 650 6111063
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1090 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-11808-3

Query Match 2.8%; Score 7; DB 5; Length 1090;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 YSQVLFQ 172
Db 787 YSQVLFQ 793

RESULT 35
US-08-804-227C-12
Sequence 12, Application US/08804227C
Patent No. 5876991
GENERAL INFORMATION:
APPLICANT: Dehoff, Bradley S.
APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Rostock, Paul R., Jr.
APPLICANT: Sulton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: USA
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII(DOS) Text only
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,227C
FILING DATE: February 21, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-8231

TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1891 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-804-227C-12

Query Match 2.8%; Score 7; DB 2; Length 1891;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 140 PALRRGR 146
Db 878 PALRRGR 884

RESULT 36
US-08-804-198-6
Sequence 6, Application US/08804198
Patent No. 5945320
GENERAL INFORMATION:
APPLICANT: Burgett, Stanley G.
APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Rao, Nagaraja R.
APPLICANT: Richardson, Mark A.
APPLICANT: Rostock, Paul R., Jr.
TITLE OF INVENTION: PLATENOILIDE SYNTHASE GENE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: PAUL R. CANTRELL 1138
STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: USA
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,198
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CANTRELL, PAUL R.
REGISTRATION NUMBER: 36,470
REFERENCE/DOCKET NUMBER: P9113
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3885
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1891 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-804-198-6

Query Match 2.8%; Score 7; DB 2; Length 1891;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 140 PALRRGR 146
Db 878 PALRRGR 884

RESULT 37
US-08-751-189-3
Sequence 3, Application US/08751189


```
/ Patent No. 5919656
/ GENERAL INFORMATION:
/ APPLICANT: Harrington, Lea A.
/ APPLICANT: Robinson, Murray O.
/ TITLE OF INVENTION: No. 5919656el Genes Encoding Telomerase Protein
/ TITLE OF INVENTION: 1
/ NUMBER OF SEQUENCES: 12
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Amgen, Inc.
/ STREET: 1840 De Havilland Drive
/ CITY: Thousand Oaks
/ STATE: California
/ COUNTRY: USA
/ ZIP: 91320-1789
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/751,189
/ FILING DATE: 15-NOV-1996
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Oleski, Nancy A.
/ REGISTRATION NUMBER: 34,688
/ REFERENCE/DOCKET NUMBER: A-433
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2627 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: unknown
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ US-08-751-189-3

Query Match          2.8%; Score 7; DB 2; Length 2627;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 PALSVAL 31
Db 1929 PALSVAL 1935

RESULT 38
US-09-060-836-3
Sequence 3, Application US/09060836
Patent No. 5981707
GENERAL INFORMATION:
APPLICANT: Harrington, Lea A.
APPLICANT: Robinson, Murray O.
TITLE OF INVENTION: No. 5981707el Genes Encoding Telomerase Protein
TITLE OF INVENTION: 1
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen, Inc.
STREET: 1840 De Havilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,836
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/751,189
```

```
/ FILING DATE: 15-NOV-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Oleski, Nancy A.
/ REGISTRATION NUMBER: 34,688
/ REFERENCE/DOCKET NUMBER: A-433
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2627 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: unknown
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ US-09-060-836-3

Query Match          2.8%; Score 7; DB 2; Length 2627;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 PALSVAL 31
Db 1929 PALSVAL 1935

RESULT 39
US-09-184-445-3
Sequence 3, Application US/09184445
Patent No. 6174703
GENERAL INFORMATION:
APPLICANT: Harrington, Lea A.
APPLICANT: Robinson, Murray O.
TITLE OF INVENTION: No. 6174703el Genes Encoding Telomerase Protein
TITLE OF INVENTION: 1
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen, Inc.
STREET: 1840 De Havilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/184,445
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/751,189
FILING DATE: 15-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Oleski, Nancy A.
REGISTRATION NUMBER: 34,688
REFERENCE/DOCKET NUMBER: A-433
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2627 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-184-445-3

Query Match          2.8%; Score 7; DB 4; Length 2627;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 PALSVAL 31
Db 1929 PALSVAL 1935
```

```
RESULT 40
US-08-751-189-4
; Sequence 4, Application US/08751189
; Patent No. 5919656
; GENERAL INFORMATION:
;   APPLICANT: Harrington, Lea A.
;   APPLICANT: Robinson, Murray O.
;   TITLE OF INVENTION: No. 5919656e1 Genes Encoding Telomerase Protein
;   TITLE OF INVENTION: 1
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Amgen, Inc.
;   STREET: 1840 De Havilland Drive
;   CITY: Thousand Oaks
;   STATE: California
;   COUNTRY: USA
;   ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/751,189
; FILING DATE: 15-NOV-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
;   NAME: Oleski, Nancy A.
;   REGISTRATION NUMBER: 34,688
;   REFERENCE/DOCKET NUMBER: A-433
; INFORMATION FOR SEQ ID NO: 4:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 2629 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: unknown
;     TOPOLOGY: unknown
;   MOLECULE TYPE: protein
; US-08-751-189-4

Query Match      2.8%; Score 7; DB 2; Length 2629;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 PALSVAL 31
Db 1936 PALSVAL 1942

SULT 41
US-09-060-836-4
; Sequence 4, Application US/09060836
; Patent No. 5981707
; GENERAL INFORMATION:
;   APPLICANT: Harrington, Lea A.
;   APPLICANT: Robinson, Murray O.
;   TITLE OF INVENTION: No. 5981707e1 Genes Encoding Telomerase Protein
;   TITLE OF INVENTION: 1
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Amgen, Inc.
;   STREET: 1840 De Havilland Drive
;   CITY: Thousand Oaks
;   STATE: California
;   COUNTRY: USA
;   ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,836
```

```
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/751,189
; FILING DATE: 15-NOV-1996
; ATTORNEY/AGENT INFORMATION:
;   NAME: Oleski, Nancy A.
;   REGISTRATION NUMBER: 34,688
;   REFERENCE/DOCKET NUMBER: A-433
; INFORMATION FOR SEQ ID NO: 4:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 2629 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: unknown
;     TOPOLOGY: unknown
;   MOLECULE TYPE: protein
; US-09-060-836-4

Query Match      2.8%; Score 7; DB 2; Length 2629;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 25 PALSVAL 31
Db 1936 PALSVAL 1942
```

```
RESULT 42
US-09-184-445-4
; Sequence 4, Application US/09184445
; Patent No. 6174703
; GENERAL INFORMATION:
;   APPLICANT: Harrington, Lea A.
;   APPLICANT: Robinson, Murray O.
;   TITLE OF INVENTION: No. 6174703e1 Genes Encoding Telomerase Protein
;   TITLE OF INVENTION: 1
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Amgen, Inc.
;   STREET: 1840 De Havilland Drive
;   CITY: Thousand Oaks
;   STATE: California
;   COUNTRY: USA
;   ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/184,445
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/751,189
; FILING DATE: 15-NOV-1996
; ATTORNEY/AGENT INFORMATION:
;   NAME: Oleski, Nancy A.
;   REGISTRATION NUMBER: 34,688
;   REFERENCE/DOCKET NUMBER: A-433
; INFORMATION FOR SEQ ID NO: 4:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 2629 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: unknown
;     TOPOLOGY: unknown
;   MOLECULE TYPE: protein
; US-09-184-445-4

Query Match      2.8%; Score 7; DB 4; Length 2629;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Oy 25 PALSVAL 31
Db 1936 PALSVAL 1942

RESULT 43

US-09-428-517-2
; Sequence 2, Application US/09428517
; Patent No. 6251636
; GENERAL INFORMATION:
; APPLICANT: Betlach, Mary C.
; APPLICANT: Shah, Sanjay Krishnakant
; APPLICANT: McDaniel, Robert
; APPLICANT: Tang, Li
; TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE
; FILE REFERENCE: 30062-20029.00
; CURRENT APPLICATION NUMBER: US/09/428,517
; CURRENT FILING DATE: 1999-10-28
; EARLIER APPLICATION NUMBER: 60/120,254
; EARLIER FILING DATE: 1999-02-16
; EARLIER APPLICATION NUMBER: 60/106,100
; EARLIER FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4150
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant
US-09-428-517-2

Query Match 2.8%; Score 7; DB 4; Length 4150;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 140 PALRGR 146
Db 882 PALRGR 888

RESULT 44

US-08-107-235-10
; Sequence 10, Application US/08107235
; Patent No. 5587457
; GENERAL INFORMATION:
; APPLICANT: Rathjen, Deborah A
; APPLICANT: Ferrante, Antonio
; APPLICANT: Widmer, Fred
; TITLE OF INVENTION: Neutrophil Stimulating Peptides
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Wilcoff, Ltd.
; STREET: 10 S. Wacker Dr.
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/107,235
; FILING DATE: 16-AUG-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,415
; FILING DATE: 12-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McDonnell, John J

REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,622A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Peptide

LOCATION: 1..15

OTHER INFORMATION: /note= "PEPTIDE 308 (54-68)"

US-08-107-235-10

Query Match 2.4%; Score 6; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 166 YSOVLF 171
Db 6 YSOVLF 11

RESULT 45

US-08-178-268-44
; Sequence 44, Application US/08178268
; Patent No. 5795859
; GENERAL INFORMATION:
; APPLICANT: RATHGEN, Deborah A
; APPLICANT: WIDMER, Fred
; APPLICANT: GRIGG, Geoffrey W
; APPLICANT: MACK, Philip O
; TITLE OF INVENTION: Peptide which Abrogates TNF and/or LPS Toxicity
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vanderhye P.C.
; STREET: 1100 No. 5795859th Glebe Road, 8th floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/178,268
; FILING DATE: 05-JAN-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: MITCHARD, Leonard C
; REGISTRATION NUMBER: 29,009
; REFERENCE/DOCKET NUMBER: 47-45
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: both
; MOLECULE TYPE: peptide
US-08-178-268-44

Query Match 2.4%; Score 6; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 YSQVLF 171
|||||
Db 6 YSQVLF 11

RESULT 46

US-08-714-960B-10
; Sequence 10, Application US/08714960B

; Patent No. 6121237

; GENERAL INFORMATION:

; APPLICANT: RATHJEN, Deborah A

; APPLICANT: FERRANTE, Antonio

; TITLE OF INVENTION: Neutrophil Stimulating Peptides

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BANNER & WITCOFF, LTD.

; STREET: 10 S. Wacker Drive, Suite 3000

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 1.44 Mb storage diskette, 3.50 inch

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: IBM compatible PC/MS-DOS

; SOFTWARE: WordPerfect version 6.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/714,960B

; FILING DATE: 17-SEP-1996

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: AU PJ9065

; FILING DATE: 12-MAR-1990

; APPLICATION NUMBER: PCT/AU91/00086

; FILING DATE: 12-MAR-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/930,415

; FILING DATE: 09-NOV-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/107,235

; FILING DATE: 16-AUG-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Resis, Robert H.

; REGISTRATION NUMBER: 32,168

; REFERENCE/DOCKET NUMBER: 92,622-B

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312) 715-1000

; TELEFAX: (312) 715-1234

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: not relevant

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: Peptide

; LOCATION: 1..15

; OTHER INFORMATION: /note= "PEPTIDE 308 (54-68) "

US-08-714-960B-10

QY 166 YSQVLF 171
|||||
Db 6 YSQVLF 11

RESULT 47
US-09-598-784-10

; Sequence 10, Application US/09598784

; Patent No. 6375928

; GENERAL INFORMATION:

; APPLICANT: RATHJEN, Deborah A

; APPLICANT: FERRANTE, Antonio

; TITLE OF INVENTION: Neutrophil Stimulating Peptides

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BANNER & WITCOFF, LTD.

; STREET: 10 S. Wacker Drive, Suite 3000

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 1.44 Mb storage diskette, 3.50 inch

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: IBM compatible PC/MS-DOS

; SOFTWARE: WordPerfect version 6.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/598,784

; FILING DATE: 21-Jun-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: AU PJ9065

; FILING DATE: 12-MAR-1990

; APPLICATION NUMBER: PCT/AU91/00086

; FILING DATE: 12-MAR-1991

; APPLICATION NUMBER: US 07/930,415

; FILING DATE: 09-NOV-1992

; APPLICATION NUMBER: US 08/107,235

; FILING DATE: 16-AUG-1993

; APPLICATION NUMBER: US 08/714,960

; FILING DATE: 17-SEP-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Resis, Robert H.

; REGISTRATION NUMBER: 32,168

; REFERENCE/DOCKET NUMBER: 11341.00001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312) 715-1000

; TELEFAX: (312) 715-1234

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: not relevant

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: Peptide

; LOCATION: 1..15

; OTHER INFORMATION: /note= "PEPTIDE 308 (54-68) "

; SEQUENCE DESCRIPTION: SEQ ID NO: 10:

US-09-598-784-10

QY 166 YSQVLF 171
|||||
Db 6 YSQVLF 11

RESULT 48
US-09-009-953-142

; Sequence 142, Application US/09009953

; Patent No. 6413517

; GENERAL INFORMATION:

; APPLICANT: Sette, Alessandro

; TITLE OF INVENTION: Identification of Broadly

; NUMBER OF SEQUENCES: 274

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,953
; FILING DATE: 21-Jan-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,713
; FILING DATE: 23-JAN-1997
; APPLICATION NUMBER: US 60/037,432
; FILING DATE: 07-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-011520US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 142:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 142:
US-09-009-953-142

Query Match 2.4%; Score 6; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 SPFLA 10
Db 1 SPFLA 6

; RESULT 49
; US-09-157-864-7
; Sequence 7, Application US/09157864
; Patent No. 6440694
; GENERAL INFORMATION:
; APPLICANT: Bienkowski, Michael J
; APPLICANT: Mills, Cynthia J
; APPLICANT: Jones, David A
; TITLE OF INVENTION: TNF-Related Death Ligand
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pharmacia & Upjohn, Intellectual Property
; ADDRESSEE: Legal Services
; STREET: 301 Henrietta Street
; CITY: Kalamazoo
; STATE: MI
; COUNTRY: USA
; ZIP: 49001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/157,864

; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerber, Lori L.
; REGISTRATION NUMBER: 41,113
; REFERENCE/DOCKET NUMBER: 6111.N CN1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 616/833-0974
; TELEFAX: 616/833-8897
; TELEX: 224401
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-157-864-7

Query Match 2.4%; Score 6; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 166 YSQVLF 171
Db 10 YSQVLF 15

; RESULT 50
; US-09-342-681C-119
; Sequence 119, Application US/09342681C
; Patent No. 6355782
; GENERAL INFORMATION:
; APPLICANT: Zonana et al.
; TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins
; FILE REFERENCE: 52978
; CURRENT APPLICATION NUMBER: US/09/342,681C
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/092,279
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: 60/112,366
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 119
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-342-681C-119

Query Match 2.4%; Score 6; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 166 YSQVLF 171
Db 12 YSQVLF 17

; RESULT 51
; US-08-690-775-1
; Sequence 1, Application US/08690775
; Patent No. 6270766
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Marc
; APPLICANT: Maini, Ravinder N.
; TITLE OF INVENTION: ANTI-TNF ANTIBODIES AND METHOTREXATE IN
; THE TREATMENT OF AUTOIMMUNE DISEASE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: TWO MILITIA DRIVE
; CITY: LEXINGTON

STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,775
FILING DATE: 01-AUG-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/607,419
FILING DATE: 28-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB94/00462
FILING DATE: 15-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/02070
FILING DATE: 06-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/958,248
FILING DATE: 08-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Brook Esq., David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: KIR92-01A4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-690-775-1

Query Match 2.4%; Score 6; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 YSQVLF 171
|||
Db 1 YSQVLF 6

RESULT 52
US-07-987-286-3
Sequence 3, Application 07/987286
Patent No. 5500366
GENERAL INFORMATION:
APPLICANT: RUSSELL-JONES, GREGORY J
APPLICANT: GECZY, ANDREW F
TITLE OF INVENTION: T-CELL EPITOPES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K STREET, N.W.
CITY: WASHINGTON, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 07/987,286
FILING DATE: 16-MAR-1993
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU91/00429
FILING DATE: 17-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PK2361
FILING DATE: 18-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: BENT, STEPHEN A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16786/175/CHAC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-987-286-3

Query Match 2.4%; Score 6; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 GAALGA 41
|||
Db 14 GAALGA 19

RESULT 53
US-08-614-626-3
Sequence 3, Application US/08614626
Patent No. 5928644
GENERAL INFORMATION:
APPLICANT: RUSSELL-JONES, GREGORY J
APPLICANT: GECZY, ANDREW F
TITLE OF INVENTION: T-CELL EPITOPES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K STREET, N.W.
CITY: WASHINGTON, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/614,626
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/987,286
FILING DATE: 16-MAR-1993
APPLICATION NUMBER: PCT/AU91/00429
FILING DATE: 17-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PK2361
FILING DATE: 18-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: BENT, STEPHEN A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16786/175/CHAC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:

LENGTH: 23 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-614-626-3

Query Match 2.4%; Score 6; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 36 GAAAGA 41
Db 14 GAAAGA 19

RESULT 54
US-07-987-286-11
Sequence 11, Application 07/987286
Patent No. 5500366

GENERAL INFORMATION:

APPLICANT: RUSSELL-JONES, GREGORY J
APPLICANT: GECZY, ANDREW F
TITLE OF INVENTION: T-CELL EPITOPES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K STREET, N.W.
CITY: WASHINGTON, D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 07/987,286
FILING DATE: 16-MAR-1993
CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/AU91/00429
FILING DATE: 17-SEP-1991
PRIOR APPLICATION DATA:

APPLICATION NUMBER: AU PK2361
FILING DATE: 18-SEP-1990

ATTORNEY/AGENT INFORMATION:
NAME: BENT, STEPHEN A.

REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16786/175/CHAC

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300

TELEFAX: 202 672 5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Modified-site

LOCATION: 1

OTHER INFORMATION: /note= "RESIDUE 1 IS PYROGLUTAMIC

OTHER INFORMATION: ACID"

FEATURE:

NAME/KEY: Modified-site

LOCATION: 25

OTHER INFORMATION: /note= "RESIDUE 25 IS CYSTEINAMIDE"

US-07-987-286-11

Query Match 2.4%; Score 6; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 36 GAAAGA 41
Db 15 GAAAGA 20

RESULT 55
US-07-987-286-24
Sequence 24, Application 07/987286
Patent No. 5500366

GENERAL INFORMATION:

APPLICANT: RUSSELL-JONES, GREGORY J
APPLICANT: GECZY, ANDREW F
TITLE OF INVENTION: T-CELL EPITOPES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K STREET, N.W.
CITY: WASHINGTON, D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 07/987,286
FILING DATE: 16-MAR-1993
CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/AU91/00429
FILING DATE: 17-SEP-1991
PRIOR APPLICATION DATA:

APPLICATION NUMBER: AU PK2361
FILING DATE: 18-SEP-1990

ATTORNEY/AGENT INFORMATION:
NAME: BENT, STEPHEN A.

REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16786/175/CHAC

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300

TELEFAX: 202 672 5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-07-987-286-24

Query Match 2.4%; Score 6; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 36 GAAAGA 41
Db 16 GAAAGA 21

RESULT 56

US-08-614-626-11

Sequence 11, Application US/08614626
Patent No. 5928644

GENERAL INFORMATION:

APPLICANT: RUSSELL-JONES, GREGORY J
APPLICANT: GECZY, ANDREW F

TITLE OF INVENTION: T-CELL EPITOPES
NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY & LARDNER

STREET: 3000 K STREET, N.W.

CITY: WASHINGTON, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/614,626
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/987,286
FILING DATE: 16-MAR-1993
APPLICATION NUMBER: PCT/AU91/00429
FILING DATE: 17-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PK2361
FILING DATE: 18-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: BENT, STEPHEN A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16786/175/CHAC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note= "RESIDUE 1 IS PYROGLUTAMIC
OTHER INFORMATION: ACID"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 25
OTHER INFORMATION: /note= "RESIDUE 25 IS CYSTEINAMIDE"
US-08-614-626-11
Query Match 2.4%; Score 6; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 36 GAALGA 41
Db 15 GAALGA 20
RESULT 57
US-08-614-626-24
Sequence 24, Application US/08614626
Patent No. 5928644
GENERAL INFORMATION:
APPLICANT: RUSSELL-JONES, GREGORY J
APPLICANT: GECZY, ANDREW P
TITLE OF INVENTION: T-CELL EPITOPES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K STREET, N.W.
CITY: WASHINGTON, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/614,626
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/987,286
FILING DATE: 16-MAR-1993
APPLICATION NUMBER: PCT/AU91/00429
FILING DATE: 17-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PK2361
FILING DATE: 18-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: BENT, STEPHEN A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16786/175/CHAC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-614-626-24
Query Match 2.4%; Score 6; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 36 GAALGA 41
Db 16 GAALGA 21
RESULT 58
US-09-230-548-20
Sequence 20, Application US/09230548
Patent No. 6326466
GENERAL INFORMATION:
APPLICANT: Bottaro, Donald P.
APPLICANT: Petryshyn, Raymond
APPLICANT: The Government of the United States of America
APPLICANT: as represented by The Secretary,
TITLE OF INVENTION: Double-Stranded RNA Dependent Protein Kinase Derived
TITLE OF INVENTION: Peptides to Promote Proliferation of Cells and Tissues
TITLE OF INVENTION: in a Controlled Manner
FILE REFERENCE: 015280-286200US
CURRENT APPLICATION NUMBER: US/09/230,548
CURRENT FILING DATE: 1999-07-23
EARLIER APPLICATION NUMBER: US 60/023,307
EARLIER FILING DATE: 1996-07-30
EARLIER APPLICATION NUMBER: WO PCT/US97/14350
EARLIER FILING DATE: 1997-07-29
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 20
LENGTH: 25
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:double-stranded
OTHER INFORMATION: RNA dependent protein kinase (PKR) peptide
OTHER INFORMATION: antagonist, cell-membrane permeable peptide
US-09-230-548-20
Query Match 2.4%; Score 6; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LLAPKG 13
| | | | |
Db 13 LLAPKG 18

RESULT 59

US-09-181-941-9
; Sequence 9, Application US/09181941
; Patent No. 6440690

GENERAL INFORMATION:

APPLICANT: Mor, Amram
Vouldoukis, Ioannis

Nicolas, Pierre

TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION
OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY

COUNTRY: USA
ZIP: 10036-2811

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows

SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/181,941

FILING DATE: 28-Oct-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/574,701

FILING DATE: 19-DEC-1995

APPLICATION NUMBER: FR 95 07831

FILING DATE: 29-JUN-1995

ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 3909-0021-999

TELEPHONE: 650-493-4935

TELEFAX: 650-493-5556

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: No. 6440690e

SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-181-941-9

Query Match 2.4%; Score 6; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 AALGAV 42
| | | | |
Db 17 AALGAV 22

RESULT 60

US-09-181-941-14
; Sequence 14, Application US/09181941
; Patent No. 6440690

GENERAL INFORMATION:

APPLICANT: Mor, Amram
Vouldoukis, Ioannis
Nicolas, Pierre

TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION
OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY

COUNTRY: USA
ZIP: 10036-2811

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows

SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/181,941

FILING DATE: 28-Oct-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/574,701

FILING DATE: 19-DEC-1995

APPLICATION NUMBER: FR 95 07831

FILING DATE: 29-JUN-1995

ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 3909-0021-999

TELEPHONE: 650-493-4935

TELEFAX: 650-493-5556

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: No. 6440690e

SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-09-181-941-14

Query Match 2.4%; Score 6; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 AALGAV 42
| | | | |
Db 24 AALGAV 29

RESULT 61

US-09-369-494-16
; Sequence 16, Application US/09369494
; Patent No. 6180607

GENERAL INFORMATION:

APPLICANT: Davies, Christopher

APPLICANT: Chen, Dadong

APPLICANT: Rocznik, Steve

TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity

FILE REFERENCE: MSB-7260

CURRENT APPLICATION NUMBER: US/09/369,494

CURRENT FILING DATE: 1999-08-05

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 16
LENGTH: 51
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: fragment from
US-09-369-494-16

Query Match 2.4%; Score 6; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 YSQVLF 171
|||||
DB 46 YSQVLF 51

RESULT 62

US-09-358-569D-14
; Sequence 14, Application US/09358569D
; Patent No. 6294648
; GENERAL INFORMATION:
; APPLICANT: Delaria, Kathy
; APPLICANT: Rocznik, Steve
; APPLICANT: Davies, Christopher
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7259
; CURRENT APPLICATION NUMBER: US/09/358,569D
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 14
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:from computer
; US-09-358-569D-14

Query Match 2.4%; Score 6; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 YSQVLF 171
|||||
DB 46 YSQVLF 51

RESULT 63

US-09-655-270A-30
; Sequence 30, Application US/09655270A
; Patent No. 6329151
; GENERAL INFORMATION:
; APPLICANT: Rouviere, Pierre E.
; TITLE OF INVENTION: High Density Sampling of Differentially Expressed Prokaryotic mR
; FILE REFERENCE: BC1011 US NA
; CURRENT APPLICATION NUMBER: US/09/655,270A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/120,702
; PRIOR FILING DATE: 1999-February-19
; PRIOR APPLICATION NUMBER: 60/152,542
; PRIOR FILING DATE: 1999-September-03
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 30
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: microbial enrichment culture-
; OTHER INFORMATION: not one single organism
US-09-655-270A-30

Query Match 2.4%; Score 6; DB 4; Length 59;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 RRAVLT 108
|||||

DB 49 RRAVLT 54

RESULT 64

US-09-247-155-112
; Sequence 112, Application US/09247155A
; Patent No. 6312922
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bouqueloret, Lydie
; TITLE OF INVENTION: Complementary DNAs
; FILE REFERENCE: GENSET.021A
; CURRENT APPLICATION NUMBER: US/09/247,155A
; CURRENT FILING DATE: 1999-02-09
; EARLIER APPLICATION NUMBER: 60/074,121
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/081,563
; EARLIER FILING DATE: 1998-04-13
; EARLIER APPLICATION NUMBER: 60/096,116
; EARLIER FILING DATE: 1998-08-10
; EARLIER APPLICATION NUMBER: 60/099,273
; EARLIER FILING DATE: 1998-10-04
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patent.pm
; SEQ ID NO 112
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -74...-1
US-09-247-155-112

Query Match 2.4%; Score 6; DB 4; Length 86;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SPFLA 10
|||||
DB 36 SPFLA 41

RESULT 65

US-08-710-749-28
; Sequence 28, Application US/08710749
; Patent No. 5955089
; GENERAL INFORMATION:
; APPLICANT: Biles, David E.
; APPLICANT: Hollingshead, Susan
; APPLICANT: Becker, Robert
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; APPLICATION DATA:
; APPLICATION NUMBER: US/08/710,749
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506

REFERENCE/DOCKET NUMBER: 454312-2074
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 amino acids
TYPE: amino acid
STRANDEDNESS: n/a
TOPOLOGY: linear
MOLECULE TYPE: amino acid
US-08-710-749-28

Query Match 2.4%; Score 6; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 SONGEG 77
|||||
53 SONGEG 58

RESULT 66
US-08-469-260A-253
Sequence 253, Application US/08469260A
Patent No. 6451578
GENERAL INFORMATION:
APPLICANT: JOHN N. SIMONS
APPLICANT: TAMI J. PILOT-MATIAS
APPLICANT: GEORGE J. DAMSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUERHOFF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUJOK
APPLICANT: ISA K. MUSHAMWAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,260A
CLASSIFICATION:
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 253:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-469-260A-253

Query Match 2.4%; Score 6; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 142 LRRGRG 147
|||||
Db 31 LRRGRG 36

RESULT 67
US-09-199-637A-353
Sequence 353, Application US/09199637A
Patent No. 6355411
GENERAL INFORMATION:
APPLICANT: Ausubel, Frederick
APPLICANT: Goodman, Howard M.
APPLICANT: Rahme, Laurence G.
APPLICANT: Mahajan-Miklos, Shalina
APPLICANT: Cao, Hui
APPLICANT: Drenkard, Eliana
APPLICANT: Tsongalis, John
TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
FILE REFERENCE: 00786/361002
CURRENT APPLICATION NUMBER: US/09/199,637A
PRIOR FILING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: 60/066,517
NUMBER OF SEQ ID NOS: 437
SOFTWARE: FastSeq for windows Version 4.0
SEQ ID NO 353
LENGTH: 122
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-199-637A-353

Query Match 2.4%; Score 6; DB 4; Length 122;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 RKRRAY 106
|||||
Db 38 RKRRAY 43

RESULT 68
US-08-858-207A-490
Sequence 490, Application US/08858207A
Patent No. 6348328
GENERAL INFORMATION:
APPLICANT: Black, Michael
APPLICANT: Hodgson, John
APPLICANT: Knowles, David
APPLICANT: Nicholas, Richard
APPLICANT: Stodola, Robert
TITLE OF INVENTION: No. 6348328e1 Compounds
CORRESPONDENCE ADDRESS: 552
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,207A

FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/017670
FILING DATE: 14-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P50475
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 490:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6348328e
08-858-207A-490

Query Match 2.4%; Score 6; DB 4; Length 127;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 RAVLTQ 109
|||
DB 107 RAVLTQ 112

RESULT 69
US-09-199-637A-371
Sequence 371, Application US/09199637A
Patent No. 6355411
GENERAL INFORMATION:
APPLICANT: Ausubel, Frederick
APPLICANT: Goodman, Howard M.
APPLICANT: Rahme, Laurence G.
APPLICANT: Mahajan-Miklos, Shalina
APPLICANT: Tan, Man-Wah
APPLICANT: Cao, Hui
APPLICANT: Drenkard, Eliana
APPLICANT: Tsongalis, John
TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
FILE REFERENCE: 00786/361002
CURRENT APPLICATION NUMBER: US/09/199,637A
CURRENT FILING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: 60/066,517
PRIOR FILING DATE: 1997-11-25
NUMBER OF SEQ ID NOS: 437
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 371
LENGTH: 129
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-199-637A-371

Query Match 2.4%; Score 6; DB 4; Length 129;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 ALSVAL 31
|||
DB 12 ALSVAL 17

RESULT 70
US-07-994-469A-10
Sequence 10, Application US/07994469A
Patent No. 5519119
GENERAL INFORMATION:

APPLICANT: Yamada, No. 5519119utoshi
APPLICANT: Kato, Masanari
APPLICANT: Miyata, Keizo
APPLICANT: Aoyama, Yoshiyuki
APPLICANT: Shikama, Hiroshi
TITLE OF INVENTION: Polypeptide
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/994,469A
FILING DATE: 21-DEC-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5519119man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 72-085-0 FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)413-3000
TELEFAX: (703)413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-994-469A-10

Query Match 2.4%; Score 6; DB 1; Length 139;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 YSQVLF 171
|||
DB 49 YSQVLF 54

RESULT 71
US-08-997-080-47
Sequence 47, Application US/08997080
Patent No. 5968524
GENERAL INFORMATION:
APPLICANT: WATSON, JAMES D.
APPLICANT: TAN, PAUL L.J.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,080
FILING DATE:
CLASSIFICATION:

```
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sleath, Janet
/ REGISTRATION NUMBER: 37,007
/ REFERENCE/DOCKET NUMBER: 11000.1007
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 206-269-0565
/ TELEFAX: 206-269-0563
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 47:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 142 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-997-080-47

Query Match
Best Local Similarity 2.4%; Score 6; DB 2; Length 142;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 GAALGA 41
DB 9 GAALGA 14

RESULT 72
US-08-997-362-47
/ Sequence 47, Application US/08997362
/ Patent No. 5985287
/ GENERAL INFORMATION:
/ APPLICANT: Tan, Paul
/ APPLICANT: Hiyama, Jun
/ APPLICANT: Visser, Elizabeth
/ APPLICANT: Skinner, Margot
/ APPLICANT: Scott, Linda
/ APPLICANT: Prestidge, Ross
/ TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
/ TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
/ NUMBER OF SEQUENCES: 194
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Law Offices of Ann W. Speckman
/ STREET: 2601 Elliott Avenue, Suite 4185
/ CITY: Seattle
/ STATE: WA
/ COUNTRY: USA
/ ZIP: 98121
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/997,362
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970
/ FILING DATE: June 12, 1997
/ APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
/ FILING DATE: August 29, 1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sleath, Janet
/ REGISTRATION NUMBER: 37,007
/ REFERENCE/DOCKET NUMBER: 11000.1002c2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 206-269-0565
/ TELEFAX: 206-269-0563
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 47:
```

```
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 142 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-997-362-47

Query Match
Best Local Similarity 2.4%; Score 6; DB 2; Length 142;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 GAALGA 41
DB 9 GAALGA 14

RESULT 73
US-08-873-970-47
/ Sequence 47, Application US/08873970
/ Patent No. 6001361
/ GENERAL INFORMATION:
/ APPLICANT: Tan, Paul
/ APPLICANT: Hiyama, Jun
/ APPLICANT: Visser, Elizabeth
/ APPLICANT: Skinner, Margot
/ APPLICANT: Scott, Linda
/ APPLICANT: Prestidge, Ross
/ TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
/ TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
/ NUMBER OF SEQUENCES: 106
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Law Offices of Ann W. Speckman
/ STREET: 2601 Elliott Avenue, Suite 4185
/ CITY: Seattle
/ STATE: WA
/ COUNTRY: USA
/ ZIP: 98121
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/873,970
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/705,347
/ FILING DATE: 29-AUG-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sleath, Janet
/ REGISTRATION NUMBER: 37,007
/ REFERENCE/DOCKET NUMBER: 11000.1002C1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 206-269-0565
/ TELEFAX: 206-269-0563
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 47:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 142 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-873-970-47

Query Match
Best Local Similarity 2.4%; Score 6; DB 3; Length 142;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 GAALGA 41
DB 9 GAALGA 14
```

Db 9 GAAAGA 14

RESULT 74

US-09-095-855-47

; Sequence 47, Application US/09095855
; Patent No. 6160093

; GENERAL INFORMATION:

; APPLICANT: Tan, Paul

; APPLICANT: Visser, Elizabeth

; APPLICANT: Skinner, Margot

; APPLICANT: Prestidge, Ross

; TITLE OF INVENTION: Compounds and Methods for

; TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections

; NUMBER OF SEQUENCES: 208

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Law Offices of Ann W. Speckman

; STREET: 2601 Elliott Avenue, Suite 4185

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98121

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/095,855

; FILING DATE:

; CLASSIFICATION:

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 08/705,347

; FILING DATE: 29-AUG-1996

; APPLICATION NUMBER: 08/873,970

; FILING DATE: 12-JUN-1997

; APPLICATION NUMBER: 08/997,362

; FILING DATE: 23-DEC-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Sleath, Janet

; REGISTRATION NUMBER: 37,007

; REFERENCE/DOCKET NUMBER: 11000.1002c3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 206-269-0565

; TELEFAX: 206-269-0563

; TELEX:

; INFORMATION FOR SEQ ID NO: 47:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 142 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-09-095-855-47

Query Match 2.4%; Score 6; DB 4; Length 142;

Best Local Similarity 100.0%; Pred. No. 3.1e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 GAAAGA 41
Db 9 GAAAGA 14

RESULT 75

US-08-705-347A-47

; Sequence 47, Application US/08705347A
; Patent No. 6284255

; GENERAL INFORMATION:

; APPLICANT: Tan, Paul

; APPLICANT: Hiyama, Jun

; APPLICANT: Visser, Elizabeth

; APPLICANT: Skinner, Margot

; APPLICANT: Scott, Linda

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND

; TITLE OF INVENTION: DIAGNOSIS OF MYCOBACTERIAL INFECTIONS

; NUMBER OF SEQUENCES: 55

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Speckman Picard PLLC

; STREET: 2601 Elliott Avenue, Suite 4185

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98121

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/705,347A

; FILING DATE: 28-AUG-1996

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Sleath, Janet

; REGISTRATION NUMBER: 37,007

; REFERENCE/DOCKET NUMBER: 11000.1002

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 206.269.0565

; TELEFAX: 206.269.0563

; INFORMATION FOR SEQ ID NO: 47:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 142 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-705-347A-47

Query Match 2.4%; Score 6; DB 4; Length 142;

Best Local Similarity 100.0%; Pred. No. 3.1e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 GAAAGA 41
Db 9 GAAAGA 14Search completed: March 26, 2003, 07:50:08
Job time : 37 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 07:42:50 ; Search time 44 Seconds
(without alignments)
546.218 Million cell updates/sec

Title: US-09-724-341-8
Perfect score: 250
Sequence: 1 MPASSPFLAPKGPNGMG.....RRAKLNLSPHGTFLGFVKL 250

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues
d size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	3.2	327	2	AB2194
2	8	3.2	645	2	A75390
3	7	2.8	27	2	A53727
4	7	2.8	76	2	T17719
5	7	2.8	78	2	B54897
6	7	2.8	94	2	S44064
7	7	2.8	101	2	C69930
8	7	2.8	106	1	GIBEP
9	7	2.8	127	2	T27873
10	7	2.8	146	2	T36476
11	7	2.8	180	2	T50598
12	7	2.8	181	2	T49759
13	7	2.8	219	2	T18797
14	7	2.8	232	1	C65197
15	7	2.8	232	2	F91233
16	7	2.8	232	2	F86080
17	7	2.8	232	2	AB0010
18	7	2.8	232	2	AC0943
19	7	2.8	252	2	F70711
20	7	2.8	255	2	AH0577
21	7	2.8	265	2	F70907
22	7	2.8	287	2	T22605
23	7	2.8	289	2	A82054
24	7	2.8	314	2	A87629
25	7	2.8	326	2	T05674
26	7	2.8	352	1	T1BOBI
27	7	2.8	359	2	T22774
28	7	2.8	364	1	UT0579
29	7	2.8	364	1	A39133

30	7	2.8	401	2	F65063	Cysteine sulfinate
31	7	2.8	401	2	F91087	hypothetical prote
32	7	2.8	401	2	H85932	hypothetical prote
33	7	2.8	421	2	AD3393	bicyclomycin resis
34	7	2.8	437	2	A72513	hypothetical prote
35	7	2.8	442	2	C87058	conserved hypothet
36	7	2.8	470	2	G70870	hypothetical prote
37	7	2.8	473	2	G69789	sugar transporter
38	7	2.8	477	2	C42214	peroxisome prolif
39	7	2.8	488	2	F86209	protein F22G5.14 l
40	7	2.8	492	1	P2WLRB	L2 protein - cotto
41	7	2.8	506	2	AF2192	bifunctional purin
42	7	2.8	587	2	S49942	hypothetical prote
43	7	2.8	588	2	T35549	hypothetical prote
44	7	2.8	601	2	T46084	CDPK-related prote
45	7	2.8	611	2	T27013	hypothetical prote
46	7	2.8	657	2	H70872	probable ctpp prot
47	7	2.8	670	2	T00083	hypothetical prote
48	7	2.8	680	2	CGHU1D	collagen alpha 1(X
49	7	2.8	705	2	T35165	probable integral
50	7	2.8	731	2	G87648	sensory box histid
51	7	2.8	771	2	F70757	probable cation tr
52	7	2.8	824	2	T44037	helicase [imported
53	7	2.8	824	2	T44222	probable helicase
54	7	2.8	860	2	C86203	hypothetical prote
55	7	2.8	1040	2	S50617	BEB1 protein - yea
56	7	2.8	1090	2	A41541	adenylate cyclase
57	7	2.8	1134	2	F87642	hypothetical prote
58	7	2.8	1245	2	H83574	conserved hypothet
59	7	2.8	1294	2	T35044	bacteriophage phiC
60	7	2.8	1347	2	F84531	probable retroelem
61	7	2.8	1446	1	A45344	immediate-early pr
62	7	2.8	1460	1	EDBEIF	hypocretin-like pr
63	7	2.8	2037	2	T16881	mycocerosate synth
64	7	2.8	2118	2	S72705	genome polypeptid
65	7	2.8	2344	1	RRWWRH	hypothetical prote
66	7	2.8	2344	2	S64740	hypothetical prote
67	7	2.8	2408	2	T24483	hypothetical prote
68	7	2.8	2629	2	T30987	telomerase-associa
69	7	2.8	2629	2	T32735	telomerase-associa
70	6	2.4	18	2	S10452	hypothetical prote
71	6	2.4	23	2	C56978	collagen alpha 1(I
72	6	2.4	43	2	C41397	hypothetical prote
73	6	2.4	55	2	A69850	hypothetical prote
74	6	2.4	63	2	C90826	hypothetical prote
75	6	2.4	71	2	C75627	hypothetical prote
76	6	2.4	74	2	T10456	dermaseptin B3 pr
77	6	2.4	77	2	T22249	hypothetical prote
78	6	2.4	78	2	T39965	ubiquitin-like pro
79	6	2.4	78	2	G86254	hypothetical prote
80	6	2.4	81	1	JN0462	adenoregulin precu
81	6	2.4	81	2	JN0710	ubiquitin-like pro
82	6	2.4	88	2	T14944	hypothetical prote
83	6	2.4	88	2	A13287	hypothetical prote
84	6	2.4	99	2	B86203	hypothetical prote
85	6	2.4	100	2	AF1490	conserved hypothet
86	6	2.4	101	2	G82648	probable glutaredo
87	6	2.4	102	2	F84709	conserved hypothet
88	6	2.4	104	2	AH0040	hypothetical prote
89	6	2.4	104	2	AC1130	hypothetical prote
90	6	2.4	107	2	T46583	ferredoxin [import
91	6	2.4	107	2	G71517	probable L21 ribos
92	6	2.4	109	2	D47056	cnr regulatory pro
93	6	2.4	111	2	C88678	protein H06H21.7 l
94	6	2.4	111	2	E85035	colicin Ia immunit
95	6	2.4	114	2	E87690	hypothetical prote
96	6	2.4	115	2	C83574	hypothetical prote
97	6	2.4	117	2	T37543	60S ribosomal prot
98	6	2.4	117	2	B75344	conserved hypothet
99	6	2.4	118	2	D82061	ribosomal protein
100	6	2.4	118	2	A11334	hypothetical prote

ALIGNMENTS

RESULT 1

AB2194

hypothetical protein alr3105 [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp.

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002

C:Accession: AB2194

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,

Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana

A:Reference number: AB1807, MUID:21595285, PMID:11759840

A:Accession: AB2194

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-327 <KUR>

A:Cross-references: GB:BA000019, PIDN:BAB74804.1, PID:g17132199, GSPDB:GN00179

A:Experimental source: strain PCC 7120

A:Genetics:

A:Gene: alr3105

Query Match

Best Local Similarity 100.0%; Score 8; DB 2; Length 327;
Pred. No. 6;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 QSSDALEA 93

Db 162 QSSDALEA 169

RESULT 2

A75390

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 DRI494 [similarity] - Deinococcus

C:Species: Deinococcus radiodurans

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Jun-2002

C:Accession: A75390

R:White, O.; Eissen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250, MUID:20036896, PMID:10567266

A:Accession: A75390

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-645 <WHI>

A:Cross-references: GB:AE001993; GB:AE000513; NID:96459244; PIDN:AAF11057.1; PID:g645925

A:Experimental source: strain R1

A:Genetics:

A:Gene: DRI494

A:Map position: 1

C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5

C:Keywords: membrane-associated complex; NAD; oxidoreductase

Query Match

Best Local Similarity 100.0%; Score 8; DB 2; Length 645;
Pred. No. 11;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 212 YSAGVFHL 219

Db 345 YSAGVFHL 352

RESULT 3

A53727

dermaseptin b - two-colored leaf frog

C:Species: Phyllomedusa bicolor (two-colored leaf frog)

C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 09-Apr-1998

C:Accession: A53727

R:Mor, A.; Amiche, M.; Nicolas, P.

Biochemistry 33, 6642-6650, 1994

A:Title: Structure, synthesis, and activity of dermaseptin b, a novel vertebrate defens

A:Reference number: A53727, MUID:94263975, PMID:8204601

A:Accession: A53727

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-27 <MOR>

C:Superfamily: dermaseptin precursor; dermorphin precursor amino-terminal homology

C:Keywords: skin

Query Match

Best Local Similarity 100.0%; Score 7; DB 2; Length 27;
Pred. No. 6.7;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 AALGAVA 43

Db 16 AALGAVA 22

RESULT 4

T17719

hypothetical protein a228R - Chlorella virus PBCV-1

C:Species: Chlorella virus PBCV-1

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T17719

R:Graves, M.V.; Van Etten, J.L.

submitted to the EMBL Data Library, May 1999

A:Reference number: Z18806

A:Accession: T17719

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-76 <GRA>

A:Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAC96596.1

A:Experimental source: specific host Chlorella strain NC64A

A:Genetics:

A:Note: a228R

Query Match

Best Local Similarity 100.0%; Score 7; DB 2; Length 76;
Pred. No. 17;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 LSVALWL 33

Db 69 LSVALWL 75

RESULT 5

B54897

dermaseptin b I precursor - two-colored leaf frog

C:Species: Phyllomedusa bicolor (two-colored leaf frog)

C:Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 16-Jul-1999

C:Accession: B54897

R:Amiche, M.; Ducancel, F.; Mor, A.; Boulain, J.C.; Menez, A.; Nicolas, P.

J. Biol. Chem. 269, 17847-17852, 1994

A:Title: Precursors of vertebrate peptide antibiotic dermaseptin b and adrenoregulin ha

A:Reference number: A54897, MUID:94299491, PMID:8074751

A:Accession: B54897

A:Molecule type: mRNA

A:Residues: 1-78 <AMI>

A:Cross-references: GB:X72387, NID:g505483, PIDN:CAA51080.1; PID:g505484

C:Superfamily: dermaseptin precursor; dermorphin precursor amino-terminal homology

C:Keywords: amidated carboxyl end; antibiotic; antifungal; skin

F;1-44/Domain: dermorphin precursor amino-terminal homology <DER>

F;1-22/Domain: signal sequence #status predicted <PRO>

F;23-44/Domain: propeptide #status predicted <SIG>

F;49-75/Product: dermaseptin b I #status experimental <MAT>

F;75/Modified site: amidated carboxyl end (Gln) (amide in mature form from following gl

Query Match

Best Local Similarity 100.0%; Score 7; DB 2; Length 78;
Pred. No. 17;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 37 AALGAVA 43
|||||||
Db 64 AALGAVA 70

RESULT 6

S44064

antifungal protein precursor - Aspergillus giganteus

C:Species: Aspergillus giganteus

C:Date: 16-Feb-1995 #sequence_revision 12-May-1995 #text_change 21-Jul-2000

C:Accession: S44064; S13203; S10314; S21865

R:Wendt, S.; Ulbrich, N.; Stahl, U.

Curt. Genet. 25, 519-523, 1994

A:Title: Molecular cloning, sequence analysis and expression of the gene encoding an anti

A:Reference number: S44064; MUID:94363778; PMID:8082203

A:Accession: S44064

A:Molecule type: DNA

A:Residues: 1-94 <MNE>

A:Cross-references: EMBL:X60771; NID:g2307; PIDN:CAA43181.1; PID:g2308

Nakaya, K.; Omata, K.; Okahashi, I.; Nakamura, Y.; Kolkenbrock, H.; Ulbrich, N.

F. J. Biochem. 193, 31-38, 1990

A:Title: Amino acid sequence and disulfide bridges of an antifungal protein isolated fro

A:Reference number: S13203; MUID:91031461; PMID:2226447

A:Accession: S13203

A:Molecule type: protein

A:Residues: 44-94 <NAK>

R:Wendt, S.; Ulbrich, N.; Stahl, U.

Nucleic Acids Res. 18, 3987, 1990

A:Title: Cloning and nucleotide sequence of a cDNA encoding the antifungal-protein of As

A:Reference number: S10314; MUID:90326523; PMID:2374718

A:Accession: S10314

A:Molecule type: mRNA

A:Residues: 20-79 <MNM>

A:Cross-references: EMBL:X53432

C:Genetics:

A:Introns: 48/3; 75/3

C:Keywords: antifungal; disulfide bond

F:1-26/Domain: signal sequence #status predicted <SIG>

F:27-43/Domain: propeptide #status predicted <PRO>

F:44-94/Product: antifungal protein #status experimental <MAT>

F:50-76, 57-83, 69-71, 92-94/Disulfide bonds: #status experimental

Query Match 2.8%; Score 7; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 37 AALGAVA 43
|||||||
Db 15 AALGAVA 21

RESULT 7

C69930

hypothetical protein yoxC - Bacillus subtilis

C:Species: Bacillus subtilis

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000

C:Accession: C69930

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertez

C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd

A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleg

teich, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel

Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon,

A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpsstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K

A:Authors: Yoshikawa, H.F.; Zumatein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A:Reference number: A69580; MUID:98044033; PMID:9384377

A:Accession: C69930

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-101 <KUN>

A:Cross-references: GB:Z99114; GB:AL009126; NID:g2634230; PIDN:CAB13744.1; PID:g2634245

A:Experimental source: strain 168

C:Genetics:

A:Gene: yoxC

C:Superfamily: Bacillus subtilis hypothetical protein yoxC

Query Match 2.8%; Score 7; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 107 LTOKOKK 113
|||||||
Db 57 LTOKOKK 63

RESULT 8

GIBEP

tegument protein - suid herpesvirus 1 (strain Rice)

C:Species: suid herpesvirus 1

A>Note: host Sus scrofa domestica (domestic pig)

C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 16-Jul-1999

R:Petrovskis, E.A.; Post, L.E.

Virology 159, 193-195, 1987

A:Title: A small open reading frame in pseudorabies virus and implications for evolutio

A:Reference number: A27815; MUID:87265472; PMID:3037781

A:Accession: A27815

A:Molecule type: DNA

A:Residues: 1-106 <PET>

A:Cross-references: GB:M16769; NID:g334041; PIDN:AAA47462.1; PID:g334042

C:Superfamily: human herpesvirus tegument protein; herpesvirus tegument protein homolog

F:48-100/Domain: herpesvirus tegument protein homology <HTP>

Query Match 2.8%; Score 7; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 8 LLAPKGP 14
|||||||
Db 30 LLAPKGP 36

RESULT 9

T27873

hypothetical protein ZK470.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000

C:Accession: T27873

R:Minx, P.

submitted to the EMBL Data Library, October 1995

A:Description: The sequence of C. elegans cosmid ZK470.

A:Reference number: Z20433

A:Accession: T27873

A:Status: preliminary; translated from GB/EMBL/DBSJ

A:Molecule type: DNA

A:Residues: 1-127 <MIN>

A:Cross-references: EMBL:U39651; PIDN:AAA80393.1; CESP:ZK470.3

C:Genetics:

A:Gene: CESP:ZK470.3

A:Introns: 17/2; 31/3; 81/1; 110/3

C:Superfamily: Caenorhabditis elegans hypothetical protein ZK470.3

Query Match 2.8%; Score 7; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 55 LQSLRRE 61
|||||||
Db 109 LQSLRRE 115

RESULT 10
T36476

hypothetical protein SCF85.16 - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C:Accession: T36476

R:Seeger, K.J.; Harris, D.; Thomson, N.R.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
Submitted to the EMBL Data Library, September 1999

A:Reference number: Z21607

A:Accession: T36476

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-146 <SEE>

A:Cross-references: EMBL:AL110470; PIDN:CAB54173.1; GSPDB:GN00070; SCOEDB:SCF85.16

A:Experimental source: strain A3(2)

C:Genetics:

A:Gene: SCOEDB:SCF85.16

Query Match

2.8%; Score 7; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 31;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 AALGAVA 43

|||||

Db 48 AALGAVA 54

RESULT 11

T50598

probable membrane protein [imported] - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000

C:Accession: T50598

R:Redenbach, M.; Kieser, H.M.; Denapalte, D.; Eichner, A.; Cullum, J.; Kinashi, H.; Hopw

Mol. Microbiol. 21, 77-96, 1996

A:Title: A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb S

A:Reference number: Z20556; MUID:97000351; PMID:8843436

A:Accession: T50598

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-180 <RED>

A:Cross-references: EMBL:AL133220; PIDN:CAB61735.1

A:Experimental source: strain A3(2)

C:Genetics:

A:Note: SCC75A.35

Query Match

2.8%; Score 7; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 37;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 GRQETLF 194

|||||

Db 173 GRQETLF 179

RESULT 12

T49759

related to microcin e492 precursor [imported] - Neurospora crassa

N:Alternate names: protein B24B19.310

C:Species: Neurospora crassa

C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000

C:Accession: T49759

R:Schulte, U.; Aign, V.; Hohelsel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,

submitted to the Protein Sequence Database, May 2000

A:Reference number: Z25022

A:Accession: T49759

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-181 <SCH>

A:Cross-references: EMBL:ALJ56192; GSPDB:GN00116; NCSP:B24B19.310

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1993

A:Experimental source: BAC clone B24B19; strain OR74A

C:Genetics:

A:Gene: NCSP:B24B19.310

A:Map position: 6

A:Introns: 52/3; 66/2; 126/1; 141/3

Query Match

2.8%; Score 7; DB 2; Length 181;
Best Local Similarity 100.0%; Pred. No. 37;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 AALGAVA 43

|||||

Db 122 AALGAVA 128

RESULT 13

T18797

hypothetical protein C01A2.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000

C:Accession: T18797

R:Kershaw, J.

Submitted to the EMBL Data Library, October 1996

A:Reference number: Z19023

A:Accession: T18797

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-219 <WIL>

A:Cross-references: EMBL:Z81029; PIDN:CAB02701.1; GSPDB:GN00019; CESP:C01A2.6

A:Experimental source: clone C01A2

C:Genetics:

A:Gene: CESP:C01A2.6

A:Map position: 1

A:Introns: 22/1; 160/3

C:Superfamily: Caenorhabditis elegans hypothetical protein C01A2.6

Query Match

2.8%; Score 7; DB 2; Length 219;
Best Local Similarity 100.0%; Pred. No. 44;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 LEAWENG 97

|||||

Db 85 LEAWENG 91

RESULT 14

C65197

transcription regulator cpxr - Escherichia coli (strain K-12)

N:Alternate names: transcription factor (cpxA 5' region)

C:Species: Escherichia coli

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Mar-2002

C:Accession: C65197; S40856; I53679; S08331

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C

.A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: C65197

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-232 <BLAT>

A:Cross-references: GB:AE000466; GB:U00096; NID:g2367328; PIDN:AAC76894.1; PID:g2367329

A:Experimental source: strain K-12, substrain MG1655

R:Plunkett III, G.; Burland, V.; Daniels, D.L.; Blattner, F.R.

Nucleic Acids Res. 21, 3391-3398, 1993

A:Title: Analysis of the Escherichia coli genome. III. DNA sequence of the region from

A:Reference number: S40802; MUID:93347969; PMID:8346018

A:Accession: S40856

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-115, 'X', 117-232 <PLU>

A:Cross-references: EMBL:L19201; NID:g304961; PIDN:AAB03045.1; PID:g305016

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1993

R:Dong, J.; Iuchi, S.; Kwan, H.S.; Lu, Z.; Lin, E.C.

Gene 136, 227-230, 1993
A>Title: The deduced amino-acid sequence of the cloned cpXR gene suggests the protein is hia coli.
A:Reference number: 153679; MUID:94124003; PMID:8294007
A:Accession: 153679
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-232 <RES>
A:Cross-references: GB:L14579; NID:g410156; PIDN:AAC36868.1; PID:g410157
R.Weber, R.F.; Silverman, P.M.
J. Mol. Biol. 203, 467-478, 1988
A>Title: The Cpx proteins of *Escherichia coli* K12. Structure of the CpxA polypeptide as
A:Reference number: S01377; MUID:89068697; PMID:3058985
A:Accession: S08331
A:Molecule type: DNA
A:Residues: 138-232 <WEB>
A:Cross-references: EMBL:X13307; NID:g41150; PIDN:CAA31686.1; PID:g41151
C:Genetics:
A:Gene: cpXR
Superfamily: ompR protein; response regulator homology
Keywords: phosphoprotein
A:11/Domain: response regulator homology <RRH>
F:51/Binding site: phosphate (Asp) (covalent) #status predicted

Query Match 2.8%; Score 7; DB 1; Length 232;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 GOVVSRE 185
|||||
Db 173 GOVVSRE 179

RESULT 15
F91233
hypothetical protein EC84838 [imported] - *Escherichia coli* (strain O157:H7, substrain R1
C:Species: *Escherichia coli*
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C:Accession: F91233
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A>Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and gene
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: F91233
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-232 <HAY>
Cross-references: GB:BA000007; PIDN:BAB38261.1; PID:g13364314; GSPDB:GN00154
Experimental source: strain O157:H7, substrain R1MD 0509952
C:Genetics:
A:Gene: EC84838
C:Superfamily: ompR protein; response regulator homology

Query Match 2.8%; Score 7; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 GOVVSRE 185
|||||
Db 173 GOVVSRE 179

RESULT 16
F86080
transcription regulator in 2-component system [imported] - *Escherichia coli* (strain O157
C:Species: *Escherichia coli*
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: F86080
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Diallanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A>Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: F86080
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-232 <STO>
A:Cross-references: GB:AE005174; NID:g1251881; PIDN:AGS9106.1; GSPDB:GN00145; UWGP:25
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: cpXR
C:Superfamily: ompR protein; response regulator homology

Query Match 2.8%; Score 7; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 GOVVSRE 185
|||||
Db 173 GOVVSRE 179

RESULT 17
AB0010
two component system response regulatory protein cpXR [imported] - *Yersinia pestis* (str
C:Species: *Yersinia pestis*
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C:Accession: AB0010
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titchall, R.W.; Holden, M.T.G.; Prentice, M.B
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett,
Nature 413, 523-527, 2001
A>Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AB0010
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-232 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC88940.1; PID:g15978187; GSPDB:GN00175
C:Genetics:
A:Gene: cpXR
C:Superfamily: ompR protein; response regulator homology

Query Match 2.8%; Score 7; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 GOVVSRE 185
|||||
Db 173 GOVVSRE 179

RESULT 18
AC0943
two-component response regulatory protein STY3812 [imported] - *Salmonella enterica* subsp.
C:Species: *Salmonella enterica* subsp. *enterica* serovar Typh
A>Note: this species has also been called *Salmonella typhi*
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
C:Accession: AC0943
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher
th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A>Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* sero
A:Reference number: AB0502; PMID:11677608
A:Accession: AC0943
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-232 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD09565.1; PID:g16504679; GSPDB:GN00176
C:Genetics:
A:Gene: STY3812
C:Superfamily: ompR protein; response regulator homology

Query Match 2.8%; Score 7; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 GQVVSRE 185
|||||
Db 173 GQVVSRE 179

RESULT 19
F70711
probable membraneprotein - Mycobacterium tuberculosis (strain H37RV)
C/Species: Mycobacterium tuberculosis
C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C/Accession: F70711
R/Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A/Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A/Reference number: A70500; MUID:98295987; PMID:9634230
A/Accession: F70711
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-252 <COL>
A/Cross-references: GB:Z79701; GB:AL123456; NID:g3261635; PIDN:CAB02041.1; PID:g1524238
A/Experimental source: strain H37RV
C/Genetics:
A/Gene: RV1491c
C/Superfamily: deda protein

Query Match 2.8%; Score 7; DB 2; Length 252;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 PVREPAL 27
|||||
Db 245 PVREPAL 251

RESULT 20
AH0577
molybdopterin-containing oxidoreductase membrane anchor chain STY0661 [imported] - Salmo
C/Species: Salmonella enterica subsp. enterica serovar Typhi
A/Note: this species has also been called Salmonella typhi
C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
A/Accession: AH0577
Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, S.; Mouton, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A/Reference number: AB0502; PMID:11677608
A/Accession: AH0577
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-255 <PAR>
A/Cross-references: GB:AL513382; PIDN:CAD05090.1; PID:g16501865; GSPDB:GN00176
C/Genetics:
A/Gene: STY0661

Query Match 2.8%; Score 7; DB 2; Length 255;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 203 HPDRAYN 209
|||||
Db 61 HPDRAYN 67

RESULT 21

F70907
hypothetical protein RV0587 - Mycobacterium tuberculosis (strain H37RV)
C/Species: Mycobacterium tuberculosis
C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C/Accession: F70907
R/Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A/Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A/Reference number: A70500; MUID:98295987; PMID:9634230
A/Accession: F70907
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-265 <COL>
A/Cross-references: GB:Z97182; GB:AL123456; NID:g3250720; PIDN:CAB09951.1; PID:g2222771
A/Experimental source: strain H37RV
C/Genetics:
A/Gene: RV0587
C/Superfamily: conserved hypothetical protein H11086

Query Match 2.8%; Score 7; DB 2; Length 265;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 GAALGAV 42
|||||
Db 92 GAALGAV 98

RESULT 22
T22605
hypothetical protein F54B11.7 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C/Accession: T22605
R/Swinburne, J.
submitted to the EMBL Data Library, March 1996
A/Reference number: Z19588
A/Accession: T22605
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-287 <WIL>
A/Cross-references: EMBL:Z70208; PIDN:CAA94139.1; GSPDB:GN00028; CESP:F54B11.7
A/Experimental source: clone F54B11
C/Genetics:
A/Gene: CESP:F54B11.7
A/Map position: X
A/Introns: 98/1; 209/3

Query Match 2.8%; Score 7; DB 2; Length 287;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 DSDVTE 135
|||||
Db 52 DSDVTE 58

RESULT 23
A82054
phosphoribulokinase VC2613 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C/Species: Vibrio cholerae
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C/Accession: A82054
R/Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A/Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A/Reference number: A82035; MUID:20406833; PMID:10952301
A/Accession: A82054

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-289 <HEI>
A:Cross-references: GB:AE004328; GB:AE003852; NID:g9657201; PIDN:AAF95754.1; GSPDB:GN001
A:Experimental source: serogroup O1, strain N16961; biotype E1 tor
C:Genetics:

A:Gene: VC2613
A:Map position: 1
C:Superfamily: phosphoribulokinase

Query Match 2.8%; Score 7; DB 2; Length 289;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 79 PMOSLPE 85
|||
Db 116 PMOSLPE 122

RESULT 24
7629

biotheoretical protein CC3067 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: A87629

R:NIerman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: A87629

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-314 <STO>

A:Cross-references: GB:AE005673; NID:g13424717; PIDN:AAK25029.1; GSPDB:GN00148

C:Genetics:

A:Gene: CC3067

Query Match 2.8%; Score 7; DB 2; Length 314;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 39 LGAVACA 45
|||
Db 4 LGAVACA 10

ULT 25
5674

Arnyestransferase homolog F20M13.20 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 26-Aug-1999

C:Accession: T05674

R:Bevan, M.; Medler, H.; Kutzner, M.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.

submitted to the Protein Sequence Database, February 1999

A:Reference number: Z15420

A:Accession: T05674

A:Molecule type: DNA

A:Residues: 1-326 <BEV>

A:Cross-references: EMBL:AL035540

A:Experimental source: cultivar Columbia; BAC clone F20M13

C:Genetics:

A:Map position: 4

A:Introns: 118/3

A:Note: F20M13.20

C:Superfamily: geranyltransferase

Query Match 2.8%; Score 7; DB 2; Length 326;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 54 ELOSLRR 60

|||||
Db 242 ELOSLRR 248

RESULT 26

TIBOBI

alpha-1-microglobulin / inter-alpha-trypsin inhibitor precursor [validated] - bovine

N:Alternate names: BI-14 (inhibitory fragment of ITI); bikunin; ITI

C:Species: Bos primigenius taurus (cattle)

C:Date: 25-Feb-1985 #sequence_revision 04-Feb-2000 #text_change 18-Aug-2000

C:Accession: S68149; A91717; A90685; S31219; A01209

R:Lindqvist, A.; Akersstroem, B.

Biochim. Biophys. Acta 1306, 98-106, 1996

A:Title: Bovine alpha(1)-microglobulin/bikunin. Isolation and characterization of liver

A:Reference number: S68149; MUID:96201710; PMID:8611630

A:Accession: S68149

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-352 <LIN>

A:Cross-references: EMBL:U35642; NID:g1016297; PIDN:AA07599.1; PID:g1016298

R:Hochstrasser, K.; Wachter, E.

Hoppe-Seyler's Z. Physiol. Chem. 364, 1679-1687, 1983

A:Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-

A:Reference number: A91717; MUID:84133807; PMID:6199275

A:Accession: A91717

A:Molecule type: protein

A:Residues: 227-267, 'L', 269-273, 'Q', 275-297, 'AF', 300-329, 'Q', 331-345, 'R', 347-348 <HOC>

R:Hochstrasser, K.; Wachter, E.; Albrecht, G.J.; Reisinger, P.

Biol. Chem. Hoppe-Seyler 366, 473-478, 1985

A:Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-

A:Reference number: A90685; MUID:85225967; PMID:2408637

A:Accession: A90685

A:Molecule type: protein

A:Residues: 347-349 <HOC2>

R:Hochstrasser, K.; Albrecht, G.J.; Schonberger, O.L.; Wachter, E.

Hoppe-Seyler's Z. Physiol. Chem. 364, 1689-1696, 1983

A:Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-

A:Reference number: A91718; MUID:84133808; PMID:6199276

A:Contents: annotation; reactive sites

R:Castillo, G.M.; Templeton, D.M.

FEBS Lett. 318, 292-296, 1993

A:Title: Subunit structure of bovine ESP (extracellular-matrix stabilizing factor(s)).

A:Reference number: S31219; MUID:93178646; PMID:7680011

A:Accession: S31219

A:Status: preliminary

A:Molecule type: protein

A:Residues: 206-214, 'X', 216, 'X', 218-220 <CAS>

C:Superfamily: protein HC; animal Kunitz-type proteinase inhibitor homology; lipocalin

C:Keywords: duplication; glycoprotein; plasma; serine proteinase inhibitor

F:35-188/Domain: lipocalin homology <LIP>

F:231-281/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>

F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>

F:241/Inhibitory site: Leu (chymotrypsin, elastase) #status experimental

F:250/Binding site: carbohydrate (Asn) (covalent) #status experimental

F:297/Inhibitory site: Arg (trypsin) #status experimental

Query Match 2.8%; Score 7; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 103 RRAVLTO 109
|||
Db 204 RRAVLTO 210

RESULT 27
T22774

hypothetical protein F56D5.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C:Accession: T22774

R:Matthews, P.

submitted to the EMBL Data Library, February 1996

A:Reference number: Z19614
A:Accession: T22774
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-359 <WIL>
A:Cross-references: EMBL:Z69662; PIDN:CAA93499.1; GSPDB:GN00022; CESP:F56DS.1
A:Experimental source: clone F56DS
C:Genetics:
A:Gene: CESP:F56DS.1
A:Map position: 4
A:Introns: 50/3; 88/1; 252/3
C:Superfamily: unassigned collagens

Query Match 2.8%; Score 7; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PKGPPGN 17
|||||
221 PKGPPGN 227

RESULT 28
JT0579
triacylglycerol lipase (EC 3.1.1.3) precursor - Pseudomonas sp.
N:Alternate names: lipase
C:Species: Pseudomonas sp.
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: JT0579; PS0202; JQ1227; PQ0229
R:Rizumi, T.; Nakamura, K.; Shimada, Y.; Sugihara, A.; Tomioka, Y.; Fukase, T.
Agric. Biol. Chem. 55, 2349-2357, 1991
A:Title: Cloning, nucleotide sequencing, and expression in Escherichia coli of a lipase
A:Reference number: JT0579; MUID:92118328; PMID:1368739
A:Accession: JT0579
A:Molecule type: DNA
A:Residues: 1-364 <IIZ>
A:Cross-references: GB:D10069; GB:D01216; NID:G216898; PIDN:BAA00960.1; PID:G216899
A:Accession: PS0202
A:Molecule type: protein
A:Residues: 45-47 <IIZ>
C:Genetics:
A:Gene: lip
C:Superfamily: Pseudomonas triacylglycerol lipase
C:Keywords: carboxylic ester hydrolase
F:1-44/Domain: signal sequence #status predicted <SIG>
F:45-364/Product: triacylglycerol lipase #status predicted <MAT>

Query Match 2.8%; Score 7; DB 1; Length 364;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GAVACAM 46
|||||
Db 12 GAVACAM 18

RESULT 29
A39133
triacylglycerol lipase (EC 3.1.1.3) precursor - Pseudomonas cepacia
C:Species: Pseudomonas cepacia
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A39133
R:Jorgensen, S.; Skov, K.W.; Diderichsen, B.
J. Bacteriol. 173, 559-567, 1991
A:Title: Cloning, sequence, and expression of a lipase gene from Pseudomonas cepacia: 11
A:Reference number: A39133; MUID:91100343; PMID:1987151
A:Accession: A39133
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-364 <JOR>
A:Cross-references: GB:M58494
C:Superfamily: Pseudomonas triacylglycerol lipase
C:Keywords: carboxylic ester hydrolase

Query Match 2.8%; Score 7; DB 1; Length 364;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GAVACAM 46
|||||
Db 12 GAVACAM 18

RESULT 30
F65063
Cysteine sulfinatase desulfinate (EC 4.4.1.-) (CSD) - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C:Accession: F65063
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: F65063
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-401 <BLAT>
A:Cross-references: GB:AE000364; GB:U00096; NID:G2367162; PIDN:AC75852.1; PID:G1789175
A:Experimental source: strain K-12, substrain MG1655
C:Superfamily: nifs protein
C:Keywords: carbon-sulfur lyase

Query Match 2.8%; Score 7; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 158 QDAGVYL 164
|||||
Db 17 QDAGVYL 23

RESULT 31
F91087
hypothetical protein ECs3670 [imported] - Escherichia coli (strain O157:H7, substrain R
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C:Accession: F91087
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: F91087
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-401 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA037093.1; PID:G13363142; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: ECs3670
C:Superfamily: nifs protein

Query Match 2.8%; Score 7; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 158 QDAGVYL 164
|||||
Db 17 QDAGVYL 23

RESULT 32,
H85932
hypothetical protein Z4127 [imported] - Escherichia coli (strain O157:H7, substrain EDL
C:Species: Escherichia coli

C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C/Accession: H85932
R/Perla, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouzis, K.; Apodaca,
Nature 409, 529-533, 2001
A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A/Reference number: AB5480; MUID:21074935; PMID:11206551
A/Accession: H85932
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-401 <STO>
A/Cross-references: GB:AE005174; NID:g12517292; PIDN:AG57924.1; GSPDB:GN00145; UWGP:Z41
A/Experimental source: strain O157:H7, substrain EDL933
C/Genetics:
A/Gene: Z4127
C/Superfamily: nifs protein

Query Match 2.8%; Score 7; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
158 QDAGVYL 164
|||||
17 QDAGVYL 23

Db 17 QDAGVYL 23

RESULT 33
AD3393
bicyclomycin resistance protein [imported] - Brucella melitensis (strain 16M)
C/Species: Brucella melitensis
C/Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
C/Accession: AD3393
R/Delvecchio, V.G.; Kaparat, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Leves
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A/Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A/Reference number: AD3252; PMID:11756688
A/Accession: AD3393
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-421 <KUR>
A/Cross-references: GB:AE008917; PIDN:AAL5231.1; PID:g17983103; GSPDB:GN00190
A/Experimental source: strain 16M
C/Genetics:
A/Gene: BME1130
A/Map position: 1
C/Superfamily: bicyclomycin resistance protein

Query Match 2.8%; Score 7; DB 2; Length 421;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
36 GAALGAV 42
|||||
368 GAALGAV 374

Db 368 GAALGAV 374

RESULT 34
A72513
hypothetical protein APE2078 - Aeropyrum pernix (strain K1)
C/Species: Aeropyrum pernix
C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C/Accession: A72513
R/Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A/Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A/Reference number: A72450; MUID:99310339; PMID:10382966
A/Accession: A72513
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-437 <KAW>
A/Cross-references: DDBJ:AF000063; NID:g5105654; PIDN:BAA81089.1; PID:g5105777

A/Experimental source: strain K1
C/Genetics:
A/Gene: APE2078
C/Superfamily: conserved hypothetical protein MTH1394

Query Match 2.8%; Score 7; DB 2; Length 437;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
227 VIIIPR 233
|||||
381 VIIIPR 387

Db 381 VIIIPR 387

RESULT 35
C87058
conserved hypothetical protein ML1193 [imported] - Mycobacterium leprae
C/Species: Mycobacterium leprae
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C/Accession: C87058
R/Cole, S.T.; Eiglmeyer, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; H
R.; Davies, R.M.; Devlin, K.; Duthey, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A/Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S
A/Title: Massive gene decay in the leprosy bacillus.
A/Reference number: A86909; MUID:21128732; PMID:11234002
A/Accession: C87058
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-442 <STO>
A/Cross-references: GB:AL450380; NID:g13093158; PIDN:CAC31574.1; GSPDB:GN00147
C/Genetics:
A/Gene: ML1193

Query Match 2.8%; Score 7; DB 2; Length 442;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
229 IPRARAK 235
|||||
306 IPRARAK 312

Db 306 IPRARAK 312

RESULT 36
G70870
hypothetical protein Rv2522c - Mycobacterium tuberculosis (strain H37RV)
C/Species: Mycobacterium tuberculosis
C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C/Accession: G70870
R/Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon,
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A/Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A/Reference number: A70500; MUID:98295987; PMID:9634230
A/Accession: G70870
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-470 <COL>
A/Cross-references: GB:AL021185; GB:AL123456; NID:g3261504; PIDN:CAA16018.1; PID:e12374
A/Experimental source: strain H37RV
C/Genetics:
A/Gene: Rv2522c

Query Match 2.8%; Score 7; DB 2; Length 470;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
229 IPRARAK 235
|||||
325 IPRARAK 331

Db 325 IPRARAK 331

RESULT 37

G69789

sugar transporter homolog ydjK - Bacillus subtilis

C/Species: Bacillus subtilis

C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000

C/Accession: G69789

R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bexter
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallier
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.;
Koeter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seroy
Leuch, M.; Tamakoshi, A.; Tanaka, T.; Terpestra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377

A/Accession: G69789

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-473 <KUN>

A/Cross-references: GB:Z99107; GB:AL009126; NID:G2632866; PIDN:CAB12442.1; PID:G2632936

A/Experimental source: strain 168

A/Genetics:

A;Gene: ydjK

C;Superfamily: glucose transport protein

Query Match 2.8%; Score 7; DB 2; Length 473;

Best Local Similarity 100.0%; Pred. No. 87;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 GAALGAV 42

Db 62 GAALGAV 68

RESULT 38

C42214

peroxisome proliferator-activated receptor gamma chain - African clawed frog

N/Alternate names: PPAR-gamma

C/Species: Xenopus laevis (African clawed frog)

C/Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 20-Sep-1999

C/Accession: C42214

R;Dreyer, C.; Krey, G.; Keller, H.; Givel, F.; Helftenbein, G.; Wahli, W.

Cell 68, 879-887, 1992

A;Title: Control of the peroxisomal beta-oxidation pathway by a novel family of nuclear

A;Reference number: A42214; MUID:92191267; PMID:1312391

A/Accession: C42214

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: nucleic acid

A/Residues: 1-477 <DRE>

A/Cross-references: GB:M84163; NID:G214667; PIDN:AAA49937.1; PID:G214668

A/Note: sequence extracted from NCBI backbone (NCBIF:88295)

C;Superfamily: unassigned erba-related proteins; erba transforming protein homology

C;Keywords: DNA binding; transcription regulation; zinc finger

F;111-395/Domain: erba transforming protein homology <ERBA>

Query Match 2.8%; Score 7; DB 2; Length 477;

Best Local Similarity 100.0%; Pred. No. 88;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 PALSVL 31

Db 283 PALSVL 289

RESULT 39

F86209

protein F22G5.14 [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C/Accession: F86209

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A/Accession: F86209

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-488 <STO>

A/Cross-references: GB:AE005172; NID:G8778543; PIDN:AAF79551.1; GSPDB:GN00141

C/Genetics:

A;Gene: F22G5.14

A;Map position: 1

Query Match 2.8%; Score 7; DB 2; Length 488;

Best Local Similarity 100.0%; Pred. No. 90;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 164 LLYSQVL 170

Db 357 LLYSQVL 363

RESULT 40

P2WLRB

L2 protein - cottontail rabbit papillomavirus

C/Species: cottontail rabbit papillomavirus

C/Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 24-Feb-1994

C/Accession: A03652

R;Giri, I.; Danos, O.; Yaniv, M.

Proc. Natl. Acad. Sci. U.S.A. 82, 1580-1584, 1985

A;Title: Genomic structure of the cottontail rabbit (Shope) papillomavirus.

A;Reference number: A94027; MUID:8516175; PMID:2984661

A/Accession: A03652

A/Molecule type: DNA

A/Residues: 1-492 <GIR>

C;Superfamily: papillomavirus L2 protein

C;Keywords: late protein

Query Match 2.8%; Score 7; DB 1; Length 492;

Best Local Similarity 100.0%; Pred. No. 91;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 99 RSRKRR 105

Db 4 RSRKRR 10

RESULT 41

AF2192

bifunctional purine biosynthesis protein [imported] - Nostoc sp. (strain PCC 7120)

C/Species: Nostoc sp.

A/Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002

C/Accession: AF2192

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,

DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An

A;Reference number: AB1807; MUID:21595285; PMID:11759840

A/Accession: AF2192

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-506 <KUR>
A:Cross-references: GB:BA000019; PIDN:BAB74792.1; PID:G17132187; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: purH
C:Superfamily: purH bifunctional enzyme

Query Match 2.8%; Score 7; DB 2; Length 506;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 53 TELOSLR 59
|||||
Db 203 TELOSLR 209

RESULT 42

9942

hypothetical protein YIL036w - yeast (Saccharomyces cerevisiae)

Alternate names: hypothetical protein YI9905.12

C:Species: Saccharomyces cerevisiae

C>Date: 13-Jan-1995 #sequence_revision 20-Feb-1995 #text_change 19-Apr-2002

C:Accession: S49942

R:Odell, C.; Bowman, S.

submitted to the EMBL Data Library, December 1994

A:Reference number: S49931

A:Accession: S49942

A:Molecule type: DNA

A:Residues: 1-587 <ODE>

A:Cross-references: GB:Z47047; EMBL:Z46861; NID:G603997; PID:G763310; GSPDB:GN00009; MIF

C:Genetics:

A:Gene: SGD:CST6; MIPS:YIL036w

A:Cross-references: SGD:S0001298

A:Map position: 9L

C:Superfamily: fos/jun DNA-binding domain homology

F/420-460/Domain: fos/jun DNA-binding domain homology <FJD>

Query Match 2.8%; Score 7; DB 2; Length 587;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 130 DSDVTEV 136
|||||
Db 530 DSDVTEV 536

RESULT 43

5549

hypothetical protein SC6G3.05 - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999

C:Accession: T35549

R:Seeger, K.J.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, July 1999

A:Reference number: Z21582

A:Accession: T35549

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-588 <SEE>

A:Cross-references: EMBL:AL096825; PIDN:CAB46977.1; GSPDB:GN00070; SCOEDB:SC6G3.05

C:Genetics:

A:Gene: SCOEDB:SC6G3.05

Query Match 2.8%; Score 7; DB 2; Length 588;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 37 AALGAFA 43
|||||
Db 538 AALGAFA 544

RESULT 44

T46084

CDPK-related protein kinase - Arabidopsis thaliana

N:Alternate names: protein T20E23.130

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Mar-2000

C:Accession: T46084

R:Bargues, M.; Perez-Perez, A.; Terol, J.; Torres, A.; Perez-Alonso, M.; Mewes, H.W.; L

submitted to the Protein Sequence Database, December 1999

A:Reference number: Z23020

A:Accession: T46084

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-601 <BAR>

A:Cross-references: EMBL:AL133363

A:Experimental source: cultivar Columbia; BAC clone T20E23

C:Genetics:

A:Map position: 3

A:Introns: 186/3; 230/2; 244/2; 280/3; 307/1; 406/1; 443/3; 479/3; 500/3; 556/3

A>Note: T20E23.130

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homol

Query Match 2.8%; Score 7; DB 2; Length 601;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 244 FLGFVKL 250
|||||
Db 583 FLGFVKL 589

RESULT 45

T27013

hypothetical protein Y48E1B.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000

C:Accession: T27013

R:McMurray, A.

submitted to the EMBL Data Library, March 1997

A:Reference number: Z20299

A:Accession: T27013

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-611 <WIL>

A:Cross-references: EMBL:Z93393; PIDN:CAB07690.1; GSPDB:GN00020; CESP:Y48E1B.4

A:Experimental source: clone Y48E1B

C:Genetics:

A:Gene: CESP:Y48E1B.4

A:Map position: 2

A:Introns: 59/2; 80/3; 144/3; 413/3

C:Superfamily: Caenorhabditis elegans hypothetical protein Y48E1B.4

Query Match 2.8%; Score 7; DB 2; Length 611;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 62 VSRLQGT 68
|||||
Db 355 VSRLQGT 361

RESULT 46

H70872

probable ctpd protein - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000

C:Accession: H70872

R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon,

; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A/Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A/Reference number: A70500; MUID:98295987; PMID:9634230
A/Accession: H70872
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-657 <COL>
A/Cross-references: GB:AL021184; GB:AL123456; NID:g3261498; PIDN:CAA15997.1; PID:g279140
A/Experimental source: strain H37Rv
A/Genetics:
C/Gene: ctpD
C/Superfamily: Enterococcus copper-transporting ATPase copB; ATPase nucleotide-binding
F:25-394/Domain: ATPase transduction domain homology <ATP>
F:465-608/Domain: ATPase nucleotide-binding domain homology <ATN>

Query Match 2.8%; Score 7; DB 2; Length 657;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

33 LSWGAL 39
|||||
26 LSWGAL 32

RESULT 47
T00083
hypothetical protein KIAA0515 - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 21-Jul-2000
C/Accession: T00083
R/Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.
DNA Res. 5, 31-39, 1998
A/Title: Prediction of the coding sequences of unidentified human genes. IX. The complete
A/Reference number: Z14086; MUID:98290545; PMID:9628581
A/Accession: T00083
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-670 <NAG>
A/Cross-references: EMBL:AB011087; NID:g3043553; PIDN:BAA25441.1; PID:g3043554
A/Experimental source: brain; clone HG0183
C/Genetics:
A/Note: KIAA0515

Query Match 2.8%; Score 7; DB 2; Length 670;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

82 SLPEOSS 88
|||||
309 SLPEOSS 315

RESULT 48
CGHUID
collagen alpha 1(X) chain precursor - human
N/Alternate names: procollagen alpha 1(X) chain
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 03-Nov-1995 #text_change 22-Jun-1999
C/Accession: S26396; S30086; S15826; S18249; A43901; I51870; S21856
R/Reichenberger, B.; Beier, F.; Luvalle, P.; Olsen, B.R.; von der Mark, K.; Bertling, W.
FEBS Lett. 311, 305-310, 1992
A/Title: Genomic organization and full-length cDNA sequence of human collagen X.
A/Reference number: S26396; MUID:93012005; PMID:1397333
A/Accession: S26396
A/Molecule type: DNA
A/Residues: 1-680 <REI>
A/Cross-references: EMBL:X68952; EMBL:X72578; EMBL:X72579; EMBL:X72580; GB:S47714; GB:S4
R/Apte, S.S.
submitted to the EMBL Data Library, March 1992
A/Reference number: S30085
A/Accession: S30086
A/Molecule type: DNA
A/Residues: 'TIPFYGMVCWVCLL', 52-680 <APT>

A/Cross-references: EMBL:X65120; NID:g23129
A/Note: the initial difference is probably due to translation of an intronic sequence
R/Apte, S.; Mattei, M.G.; Olsen, B.R.
FEBS Lett. 282, 393-396, 1991
A/Title: Cloning of human alpha-1(X) collagen DNA and localization of the COL10A1 gene
A/Reference number: S15826; MUID:91243838; PMID:2037056
A/Accession: S15826
A/Molecule type: DNA
A/Residues: 561-647, 'G', 649-666 <AP2>
A/Cross-references: EMBL:X58879; NID:g30013; PIDN:CAA41686.1; PID:g30014
R/Thomas, J.T.; Cresswell, C.J.; Rash, B.; Nicolai, H.; Jones, T.; Solomon, E.; Grant, J.
Biochem. J. 280, 617-623, 1991
A/Title: The human collagen X gene. Complete primary translated sequence and chromosomal
A/Reference number: S18249; MUID:92109659; PMID:1764025
A/Accession: S18249
A/Molecule type: DNA
A/Residues: 1-26, 'T', 28-680 <THO>
A/Cross-references: EMBL:X60382; NID:g30094; PIDN:CAA42933.1; PID:g30095
A/Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 532-A1
R/Reichenberger, E.; Aigner, T.; von der Mark, K.; Stoss, H.; Bertling, W.
Dev. Biol. 148, 562-572, 1991
A/Title: In situ hybridization studies on the expression of type X collagen in fetal hu
A/Reference number: A43901; MUID:92077285; PMID:1743401
A/Accession: A43901
A/Molecule type: mRNA
A/Residues: 547-656 <RE2>
A/Cross-references: GB:M74050; GB:D57494; NID:g339884; PIDN:AAA61221.1; PID:g553796
A/Note: sequence extracted from NCBI backbone (NCBIN:69012, NCBI:69014)
R/Mallis, G.A.; Rash, B.; Sweetman, W.A.; Thomas, J.T.; Super, M.; Evans, G.; Grant, M.
Am. J. Hum. Genet. 54, 169-178, 1994
A/Title: Amino acid substitutions of conserved residues in the carboxyl-terminal domain
pe Schmid.
A/Reference number: I51870; MUID:94136476; PMID:8304336
A/Accession: I51870
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 520-597, 'D', 599-680 <WAL>
A/Cross-references: GB:S68531; NID:g545180; PIDN:AAC60615.1; PID:g545181
A/Note: a second mutant sequence from patient with metaphyseal chondrodysplasia type Schmid
A/Note: a mutant sequence with 614-Pro is also described
C/Comment: Prolines and lysines at the third position of the tripeptide repeating unit
ed and subsequently O-glycosylated.
C/Genetics:
A/Gene: GDB:COL10A1
A/Cross-references: GDB:128635; OMIM:120110
A/Map position: 6q21-6q22
A/Introns: 52/1
A/Note: a defect in this gene may cause Schmid metaphyseal chondrodysplasia
C/Complex: type X collagen may be a homotrimer
C/Function:
A/Description: structural component of extracellular fibrous polymer specifically and t
be important for skeletogenesis
C/Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
C/Keywords: coiled coil; extracellular matrix; glycoprotein; homotrimer; hydroxyllysine;
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-680/Product: collagen alpha 1(X) chain #status predicted <MAT>
F:19-56/Domain: amino-terminal nonhelical #status predicted <NC2>
F:57-519/Region: interrupted helical
F:520-680/Domain: amino-terminal nonhelical #status predicted <NC1>
F:553-679/Domain: complement C1q carboxyl-terminal homology <C1Q>
F:617/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 2.8%; Score 7; DB 1; Length 680;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GPPGNMG 19
|||||
DB 338 GPPGNMG 344

RESULT 49
T35165

probable integral membrane protein - Streptomyces coelicolor

C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C:Accession: T35165
R:Seeger, K.J.; Harris, D.; Parkhill, J.; Barrrell, B.G.; Rajandream, M.A.
Submitted to the EMBL Data Library, July 1998
A:Reference number: Z21570
A:Accession: T35165
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-705 <SEE>
A:Cross-references: EMBL:AL031107; PIDN:CAA19945.1; GSPDB:GN00070; SCOEDB:SC5A7.16c
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SC5A7.16c

Query Match
Best Local Similarity 2.8%; Score 7; DB 2; Length 705;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

36 GAALGAV 42
|||||||
Db 537 GAALGAV 543

RESULT 50
G87648
benzoyl box histidine kinase/response regulator [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: G87648
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
N., J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: G87648
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-731 <STO>
A:Cross-references: GB:AE005673; NID:g13424907; PIDN:AAK25187.1; GSPDB:GN00148
C:Genetics:
A:Gene: CC3225

Query Match
Best Local Similarity 2.8%; Score 7; DB 2; Length 731;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

169 VLFOVDVT 175
|||||||
Db 311 VLFOVDVT 317

RESULT 51
F70757
probable cation transport ATPase - Mycobacterium tuberculosis (strain H37Rv)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: F70757
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
; Connor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: F70757
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-771 <COL>
A:Cross-references: GB:Z74025; GB:AL123456; NID:g3261586; PIDN:CAA98411.1; PID:g3261588
A:Experimental source: strain H37Rv

C:Genetics:
A:Gene: ctgG
C:Superfamily: Enterococcus copper-transporting ATPase copB; ATPase nucleotide-binding
F:167-507/Domain: ATPase transduction domain homology <ATT>
F:575-717/Domain: ATPase nucleotide-binding domain homology <ATN>

Query Match
Best Local Similarity 2.8%; Score 7; DB 2; Length 771;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 AALGAVA 43
|||||||
Db 218 AALGAVA 224

RESULT 52
T44037
helicase [imported] - human herpesvirus 6 (strain HST)
C:Species: human herpesvirus 6
A:Variety: strain HST
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C:Accession: T44037
R:Isegawa, Y.; Mukai, T.; Nakano, K.; Kagawa, M.; Chen, J.; Mori, Y.; Sunagawa, T.; Kaw
J. Virol. 73, 8053-8063, 1999
A:Title: Comparison of the complete DNA sequences of human herpesvirus 6 variants A and
A:Accession: T44037
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-824 <ISE>
A:Cross-references: EMBL:AB021506; NID:g4995977; PIDN:BAA78298.1; PID:g4996065
A:Experimental source: strain HST; pop. variant B
C:Genetics:
A:Note: U77
C:Superfamily: varicella-zoster virus gene 55 protein

Query Match
Best Local Similarity 2.8%; Score 7; DB 2; Length 824;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 ALGAVAC 44
|||||||
Db 186 ALGAVAC 192

RESULT 53
T44222
probable helicase (EC 3.6.1.-) U77 [similarity] - human herpesvirus 6 (strain Z29)
C:Species: human herpesvirus 6
A:Variety: strain Z29
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 05-May-2000
C:Accession: T44222
R:Dominguez, G.; Dambaugh, T.R.; Stamey, F.R.; Dewhurst, S.; Inoue, N.; Pellett, P.E.
J. Virol. 73, 8040-8052, 1999
A:Title: Human herpesvirus 6B genome sequence: coding content and comparison with human
A:Reference number: Z22734; MUID:99412318; PMID:10482553
A:Accession: T44222
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-824 <DOM>
A:Cross-references: EMBL:AF157706; PIDN:AB06360.1
A:Experimental source: strain Z29; variant B
C:Genetics:
A:Note: U77
C:Superfamily: varicella-zoster virus gene 55 protein
C:Keywords: hydrolase

Query Match
Best Local Similarity 2.8%; Score 7; DB 2; Length 824;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 ALGAVAC 44
|||||||

Db 186 ALGAVAC 192

RESULT 54

C86203

hypothetical protein [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C/Accession: C86203

R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Cressy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A/Reference number: A86141; MUID:21016719; PMID:11130712

C/Accession: C86203

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-860 <STO>

A/Cross-references: GB:AE005172; NID:g7523712; PIDN:AAF63151.1; GSPDB:GN00141

C/Genetics:

A/Map position: 1

Query Match 2.8%; Score 7; DB 2; Length 860;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 190 QETLFR 196

|||||

Db 558 QETLFR 564

RESULT 55

S50617

BEB1 protein - yeast (Saccharomyces cerevisiae)

N/Alternate names: protein YER114C

C/Species: Saccharomyces cerevisiae

C/Date: 28-Jan-1995 #sequence_revision 12-May-1995 #text_change 20-Jun-2000

C/Accession: S50617; S48300

R/Dietrich, F.S.

Submitted to the EMBL Data Library, December 1994

A/Description: The sequence of S. cerevisiae cosmids 9781, 8198, 9115, 9981, and lambda

A/Reference number: S50617

C/Accession: S50617

A/Molecule type: DNA

A/Residues: 1-1040 <DIE>

A/Cross-references: EMBL:U18916; NID:g1384128; PIDN:AAC03212.1; PID:g603353; MIPS:YER114

R/Matsumi, Y.; Matsumi, R.; Toh-e, A.

Submitted to the EMBL Data Library, September 1994

A/Description: The yeast gene BEB1, encoding a protein that binds Bem1p, is involved in

A/Reference number: S48300

A/Accession: S48300

A/Molecule type: DNA

A/Residues: 1-732, 'A', 734-1040 <MAT>

A/Cross-references: EMBL:D38310; NID:g550094; PIDN:BAA07427.1; PID:g550095

C/Genetics:

A/Gene: SGD:BOI2; BEB1

A/Cross-references: MIPS:YER114C; SGD:S0000916

A/Map position: 5R

C/Superfamily: BEB1 protein-binding protein BOB1, pleckstrin repeat homology; SAM homolo

F;50-102/Domain: SH3 homology <SH3>

F;263-329/Domain: SAM homology <SAM>

Query Match 2.8%; Score 7; DB 2; Length 1040;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SSPFLA 10

Db 993 SSPFLA 999

RESULT 56

A41541

adenylate cyclase (EC 4.6.1.1) II - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jul-1999

C/Accession: A41541

R/Feinstein, P.G.; Schrader, K.A.; Bakalyar, H.A.; Tang, W.J.; Krupinski, J.; Gilman, A

Proc. Natl. Acad. Sci. U.S.A. 88, 10173-10177, 1991

A/Title: Molecular cloning and characterization of a Ca(2+)/calmodulin-insensitive aden

A/Reference number: A41541; MUID:92052233; PMID:1719547

A/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <FEI>

A/Cross-references: GB:M80550; NID:g202751; PIDN:AAA40682.1; PID:g202752

C/Superfamily: human adenylate cyclase; guanylate cyclase catalytic domain homology

C/Keywords: phosphorus-oxygen lyase; transmembrane protein

F;222-466/Domain: guanylate cyclase catalytic domain homology <GCC>

F;834-1079/Domain: guanylate cyclase catalytic domain homology <GCC2>

Query Match 2.8%; Score 7; DB 2; Length 1090;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 YSQVLFQ 172

|||||

Db 787 YSQVLFQ 793

RESULT 57

F87642

hypothetical protein CC3176 [imported] - Caulobacter crescentus

C/Species: Caulobacter crescentus

C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001

C/Accession: F87642

R/Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J

B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolo

n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A/Title: Complete Genome Sequence of Caulobacter crescentus.

A/Reference number: A87249; MUID:21173698; PMID:11259647

A/Accession: F87642

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1134 <STO>

A/Cross-references: GB:AE005673; NID:g13424848; PIDN:AAK25138.1; GSPDB:GN00148

C/Genetics:

A/Gene: CC3176

Query Match 2.8%; Score 7; DB 2; Length 1134;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LLAPKGP 14

|||||

Db 1021 LLAPKGP 1027

RESULT 58

H83574

conserved hypothetical protein PA0575 [imported] - Pseudomonas aeruginosa (strain PA01)

C/Species: Pseudomonas aeruginosa

C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C/Accession: H83574

R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Latbig, K.; Lim

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path

A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: H83574
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1245 <STO>
A:Cross-references: GB:AE004493; GB:AE004091; NID:g9946436; PIDN:AAG03964.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA0575

Query Match 2.8%; Score 7; DB 2; Length 1245;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 LRREVS 64
|||||
Db 293 LRREVS 299

RESULT 59

Microphage phiC31 resistance protein pglY - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 01-Dec-2000
C:Accession: T35044; T30203
R:Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
Submitted to the EMBL Data Library, August 1998
A:Reference number: Z21566
A:Accession: T35044
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1294 <SEE>

A:Cross-references: EMBL:AL031371; PIDN:CAA20546.1; GSPDB:GN00070; SCOEDB:SC4G2.09
A:Experimental source: strain A3(2)
R:Bedford, D.J.; Laitly, C.; Butner, M.J.
J. Bacteriol. 177, 4681-4689, 1995
A:Title: Two genes involved in the phase-variable phi C31 resistance mechanism of Strept
A:Reference number: Z20777; MUID:95370146; PMID:7642495
A:Accession: T30203
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-372, 'N', 374-913, 'I', 915-1002, 'A', 1004-1294 <BED>
A:Cross-references: EMBL:L37531; NID:g576537; PID:g576538; PIDN:AAB00365.1
C:Genetics:
A:Gene: pglY; SCOEDB:SC4G2.09

Query Match 2.8%; Score 7; DB 2; Length 1294;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 140 PALRRGR 146
|||||
Db 1040 PALRRGR 1046

RESULT 60

probable retroelement pol polyprotein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C:Accession: F84531
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Mofatt, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;
euser, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: F84531
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1347 <STO>
A:Cross-references: GB:AE002093; NID:g4335731; PIDN:AAD17409.1; GSPDB:GN00139
C:Genetics:

A:Gene: AC2915650
A:Map position: 2
C:Superfamily: retrovirus-related polyprotein

Query Match 2.8%; Score 7; DB 2; Length 1347;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 LOSLRRE 61
|||||
Db 115 LOSLRRE 121

RESULT 61

A45344
immediate-early protein - suid herpesvirus 1 (strain Kaplan)
C:Species: suid herpesvirus 1
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C:Accession: A45344
R:Vlcek, C.; Kozmik, Z.; Paces, V.; Schlrm, S.; Schwyzler, M.
Virology 179, 365-377, 1990
A:Title: Pseudorabies virus immediate-early gene overlaps with an oppositely oriented o
A:Reference number: A45344; MUID:91021039; PMID:2171211
A:Accession: A45344
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-1446 <VLC>
A:Cross-references: GB:M34651; NID:g334070; PIDN:AAA47470.1; PID:g334071
C:Superfamily: herpesvirus immediate-early protein IE175
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 2.8%; Score 7; DB 1; Length 1446;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 ALRRGRG 147
|||||
Db 339 ALRRGRG 345

RESULT 62

EDBEIF
immediate-early protein IE180 - suid herpesvirus 1 (strain Indiana-Funkhauser)
C:Species: suid herpesvirus 1
C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 16-Feb-1997
C:Accession: S04713
R:Cheung, A.K.
Nucleic Acids Res. 17, 4637-4646, 1989
A:Title: DNA nucleotide sequence analysis of the immediate-early gene of pseudorabies v
A:Reference number: S04713; MUID:89315207; PMID:2546124
A:Accession: S04713
A:Molecule type: DNA
A:Residues: 1-1460 <CHE>
C:Superfamily: herpesvirus immediate-early protein IE175
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 2.8%; Score 7; DB 1; Length 1460;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 ALRRGRG 147
|||||
Db 347 ALRRGRG 353

RESULT 63

TI6881
hypothetical protein TI6812.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: TI6881
R:Wilcox, L.
Submitted to the EMBL Data Library, November 1995

A;Description: The sequence of C. elegans cosmid T14G12.
A;Reference number: Z18596
A;Accession: T16881
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-2037 <WIL>
A;Cross-references: EMBL:U41268; NID:g1086843; PID:g1086848; PIDN:AAA82437.1; CESP:T14G12
C;Genetics:
A;Gene: CESP:T14G12.5
A;Introns: 715/2; 1484/2

Query Match 2.8%; Score 7; DB 2; Length 2037;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 ASSPFL 9
|||||
Db 1060 ASSPFL 1066

RESULT 64

mycocerosate synthase (EC 2.3.1.111) - Mycobacterium leprae
N;Alternate names: Lepb1170 G2_209 protein
C;Species: Mycobacterium leprae
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-May-2000
C;Accession: S72705
R;Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, November 1993
A;Description: Mycobacterium leprae cosmid B1170.
A;Reference number: S72693
A;Accession: S72705
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2118 <SMI>
A;Cross-references: EMBL:U00010; NID:g466780; PIDN:AAA17069.1; PID:g466793
C;Genetics:
A;Start codon: TTG
A;Superfamily: mycocerosic acid synthase; 3-oxoacyl-[acyl-carrier-protein] synthase I hcnase homology; [acyl-carrier-protein] S-malonyltransferase homology
C;Keywords: acyltransferase; carrier protein; coenzyme A
F;28-426/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>
F;536-816/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT>
F;1449-1738/Domain: long-chain alcohol dehydrogenase homology <LADH>
F;1770-1954/Domain: short-chain alcohol dehydrogenase homology <SADH>
F;2038-2110/Domain: acyl carrier protein homology <ACPL>

Query Match 2.8%; Score 7; DB 2; Length 2118;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 140 PALRRGR 146
|||||
Db 1294 PALRRGR 1300

RESULT 65

RRWMRH
genome polypeptide - rabbit hemorrhagic disease virus
N;Contains: RNA-directed RNA polymerase (EC 2.7.7.48)
C;Species: rabbit hemorrhagic disease virus
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 29-May-1998
C;Accession: A41039
R;Meyers, G.; Wirblich, C.; Thiel, H.J.
Virology 184, 664-676, 1991
A;Title: Rabbit hemorrhagic disease virus--molecular cloning and nucleotide sequencing
A;Reference number: A41039; MUID:91361557; PMID:1840711
A;Accession: A41039
A;Molecule type: Genomic RNA
A;Residues: 1-2344 <MEY>
A;Cross-references: GB:M67473
C;Superfamily: rabbit calicivirus RNA-directed RNA polymerase
C;Keywords: nucleotidyltransferase

Query Match 2.8%; Score 7; DB 1; Length 2344;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 37 AALGAVA 43
|||||
Db 982 AALGAVA 988

RESULT 66

S64740
genome polypeptide - rabbit hemorrhagic disease virus (isolate AST/89)
N;Contains: VP60 protein
C;Species: rabbit hemorrhagic disease virus
A;Variety: isolate AST/89
C;Date: 12-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 20-Jun-2000
C;Accession: S64740; S46944; S49018; S65012
R;Casals, R.; Martin-Alonso, J.; Boga, J.; Parra, F.
submitted to the EMBL Data Library, May 1995
A;Description: Genomic organization of rabbit hemorrhagic disease virus determined by dA;Reference number: S64740
A;Accession: S64740
A;Molecule type: genomic RNA
A;Residues: 1-2344 <CAS>
A;Cross-references: EMBL:Z49271; NID:g1182032; PIDN:CAA89265.1; PID:g1150552
A;Experimental source: isolate AST/89
R;Boga, J.; Casals, R.; Marin, M.; Martin-Alonso, J.; Carmenes, R.; Prieto, M.; Parra, submitted to the EMBL Data Library, July 1993
A;Description: Molecular cloning, sequence and expression of the capsid protein gene frA;Reference number: S46944
A;Accession: S46944
A;Molecule type: genomic RNA
A;Residues: 1650-2344 <BOG>
A;Cross-references: EMBL:Z24757; NID:g515622; PIDN:CAA80881.1; PID:g515623
A;Experimental source: isolate AST/89
R;Parra, F.; Boga, J.A.; Marin, M.S.; Casals, R.
Virus Res. 27, 219-228, 1993
A;Title: The amino terminal sequence of VP60 from rabbit hemorrhagic disease virus suppA;Reference number: S49018; MUID:93255896; PMID:8488721
A;Accession: S49018
A;Molecule type: genomic RNA
A;Residues: 1650-1796 <PAR>
A;Cross-references: EMBL:Z24757
A;Experimental source: isolate AST/89
A;Accession: S65012
A;Molecule type: protein
A;Residues: 1767-1779;1875-1877,'X',1879-1881;1936-1938,'X',1940-1941 <PAW>
C;Superfamily: rabbit calicivirus RNA-directed RNA polymerase
C;Keywords: blocked amino end; polypeptide

Query Match 2.8%; Score 7; DB 2; Length 2344;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 37 AALGAVA 43
|||||
Db 982 AALGAVA 988

RESULT 67

T24483
hypothetical protein T05A1.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C;Accession: T24483
R;Lloyd, C.
submitted to the EMBL Data Library, December 1995
A;Reference number: Z19897
A;Accession: T24483
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-2408 <WIL>

A:Cross-references: EMBL:Z68219; PIDN:CAA92477.1; GSPDB:GN00022; CESP:T05A1.4
A:Experimental source: clone T05A1
C:Genetics:
A:Gene: CESP:T05A1.4
A:Map position: 4
A:Insertions: 817/1; 1320/2; 1598/1; 1879/3
C:Superfamily: Caenorhabditis elegans hypothetical protein ZK228.2

Query Match 2.8%; Score 7; DB 2; Length 2408;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 ASSPFL 9
|||||
Db 1329 ASSPFL 1335

RESULT 68
T30987

telomerase-associated protein 1 - mouse
Species: Mus musculus (house mouse)
Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C:Accession: T30987

R:Harrington, L.; McPhail, T.; Mar, V.; Zhou, W.; Oulton, R.; Baas, M.B.; Arruda, I.; Ro
Science 275, 973-977, 1997
A:Title: A mammalian telomerase-associated protein.
A:Reference number: Z20952; MUID:97172559; PMID:9020079
A:Accession: T30987
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2629 <HAR>
A:Cross-references: EMBL:U86137; NID:G1835783; PID:G1835784; PIDN:AAC53043.1

Query Match 2.8%; Score 7; DB 2; Length 2629;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 25 PALSVAL 31
|||||
Db 1936 PALSVAL 1942

RESULT 69
T32735

telomerase-associated protein component 1 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
A:Accession: T32735

Nakayama, J.; Saito, M.; Nakamura, H.; Matsuura, A.; Ishikawa, F.
J Biol Chem 269, 875-884, 1997
A:Title: TLPI: a gene encoding a protein component of mammalian telomerase is a novel me
A:Reference number: Z21217; MUID:97236507; PMID:9118230
A:Accession: T32735
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2629 <NAK>
A:Cross-references: EMBL:U89282; NID:G1932816; PID:G1932817; PIDN:AAB51690.1
A:Experimental source: strain Fischer 344
C:Genetics:
A:Gene: TLPI
C:Function:

A:Description: modification of telomerase-associated protein component 1 may regulate te

Query Match 2.8%; Score 7; DB 2; Length 2629;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 25 PALSVAL 31
|||||
Db 1940 PALSVAL 1946

RESULT 70

S10452
hypothetical protein (bpha 5' region) - Aspergillus niger
C:Species: Aspergillus niger
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Sep-1997
R:van Gorcom, R.F.M.; Boschloo, J.G.; Kuijvenhoven, A.; Lange, J.; Bos, C.J.; van Balke
submitted to the EMBL Data Library, March 1990
A:Reference number: S10452

A:Accession: S10452
A:Molecule type: DNA
A:Residues: 1-18 <VAN>
A:Cross-references: EMBL:X52521; NID:G2336; PID:G2337

Query Match 2.4%; Score 6; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 189 ROETLF 194
|||||
Db 8 ROETLF 13

RESULT 71
C56978

collagen alpha 1(II) chain - bovine (fragment)
N:Alternate names: collagen alpha 3(XI) chain
C:Species: Bos primigenius taurus (cattle)
C:Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 05-Dec-1998
C:Accession: C56978
R:Wu, J.J.; Eyre, D.R.
J. Biol. Chem. 270, 18865-18870, 1995
A:Title: Structural analysis of cross-linking domains in cartilage type XI collagen. In:
A:Reference number: A56978; MUID:95370194; PMID:7642541
A:Accession: C56978
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-23 <WUA>
C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology
C:Keywords: hydroxylysine; hydroxyproline
F:5/Modified site: 5-hydroxylysine (Lys) (partial) #status experimental
F:8/Modified site: 4-hydroxyproline (Pro) #status experimental

Query Match 2.4%; Score 6; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 PKGPPG 16
|||||
Db 4 PKGPPG 9

RESULT 72
C41397

hypothetical protein 2 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 03-May-1994
C:Accession: C41397
R:Miller, D.A.; Lee, A.; Matsui, Y.; Chen, E.Y.; Moses, H.L.; Derynck, R.
Mol. Endocrinol. 3, 1926-1934, 1989
A:Title: Complementary DNA cloning of the murine transforming growth factor-beta3 (TGFB;
t tissues.
A:Reference number: A41397; MUID:90190650; PMID:2628730

A:Accession: C41397
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-43 <MTL>
A:Cross-references: GB:M32745

Query Match 2.4%; Score 6; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 SSPFL 9

|||||
Db 19 SSPFL 24

RESULT 73

hypo9850

hypothetical protein yjfb - Bacillus subtilis

C/Species: Bacillus subtilis

C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999

C/Accession: A69850

R/Kunt, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bester
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997

A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.;
Koeter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A/Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mausel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
leger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot
leucht, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A/Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A/Reference number: A69580; MUID:98044033; PMID:9384377

A/Accession: A69850

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-55 <KUN>

A/Cross-references: GB:Z99110; GB:AL009126; NID:g2633472; PIDN:CAB13069.1; PID:el183232;

A/Experimental source: strain 168

C/Genetics:

A/Gene: yjfb

Query Match 2.4%; Score 6; DB 2; Length 55;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 PALSVA 30

Db 4 PALSVA 9

RESULT 74

C90826

hypothetical protein ECS1579 [imported] - Escherichia coli (strain O157:H7, substrain R1

C/Species: Escherichia coli

C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001

C/Accession: C90826

R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001

A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc

A/Reference number: A99629; MUID:21156231; PMID:11258796

A/Accession: C90826

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-63 <HAY>

A/Cross-references: GB:BA000007; PIDN:BA035002.1; PID:g13361043; GSPDB:GN00154

A/Experimental source: strain O157:H7, substrain R1MD 0509952

C/Genetics:

A/Gene: ECS1579

Query Match 2.4%; Score 6; DB 2; Length 63;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 SVALWL 33

Db 48 SVALWL 53

RESULT 75

C75627

hypothetical protein - Deinococcus radiodurans (strain R1)

C/Species: Deinococcus radiodurans

C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000

C/Accession: C75627

R/White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
S.; Shen, M.; Vamathevan, J.U.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999

A/Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A/Reference number: A75250; MUID:20036896; PMID:10567266

A/Accession: C75627

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-71 <WHI>

A/Cross-references: GB:AE001826; NID:g6460827; PIDN:AAF12650.1; PID:g6460946; TIGR:DRB0

A/Experimental source: strain R1

C/Genetics:

A/Gene: DRB0085

A/Map position: megaplasmid

A/Genome: plasmid

A/Note: plasmid MP1

Query Match 2.4%; Score 6; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 162 VYLXYS 167

Db 59 VYLXYS 64

Search completed: March 26, 2003, 07:49:38
Job time : 58 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 07:37:00 ; Search time 87 Seconds
(without alignments)
592.089 Million cell updates/sec

Title: US-09-724-341-8
Perfect score: 250
Sequence: 1 MPASSPFLAPKGPNGMG.....RAKLNLSPHGTFLGFVKL 250

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

rd size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	3.2	202	16 Q8RE60	Q8RE60 fusobacteri
2	8	3.2	223	10 Q94A36	Q94A36 arabidopsis
3	8	3.2	327	16 Q8YS10	Q8YS10 anabaena sp
4	8	3.2	577	16 Q8REN2	Q8REN2 thermoaer
5	8	3.2	645	16 Q9RU98	Q9RU98 deinococcus
6	8	3.2	773	13 P79805	P79805 morone saxa
7	7	2.8	76	12 Q84548	Q84548 paramedium
8	7	2.8	79	5 O96487	O96487 plasmodium
9	7	2.8	90	6 Q9N0A0	Q9N0A0 macaca fasc
10	7	2.8	106	8 Q9MFF2	Q9MFF2 beta vulgar
11	7	2.8	106	12 Q91GK6	Q91GK6 pseudorabie
12	7	2.8	122	11 Q9CQB7	Q9CQB7 mus musculu
13	7	2.8	127	5 Q23503	Q23503 caenorhabdi
14	7	2.8	129	10 Q94FPI	Q94FPI oryza sativ
15	7	2.8	142	10 Q941A6	Q941A6 arabidopsis
16	7	2.8	146	16 Q9S2C5	Q9S2C5 streptomyce

17	7	2.8	156	2 Q9S6G3	Q9S6G3 streptococc
18	7	2.8	156	2 Q9S6G4	Q9S6G4 streptococc
19	7	2.8	170	11 Q9DAF5	Q9DAF5 mus musculu
20	7	2.8	175	17 Q8ZWM1	Q8ZWM1 pyrobaculum
21	7	2.8	180	16 Q9RKN9	Q9RKN9 streptomyce
22	7	2.8	183	10 Q9FSU6	Q9FSU6 fagus sylvia
23	7	2.8	185	10 Q8S7G3	Q8S7G3 oryza sativ
24	7	2.8	192	11 Q9D5L5	Q9D5L5 mus musculu
25	7	2.8	193	11 Q9D9T6	Q9D9T6 mus musculu
26	7	2.8	200	2 Q30656	Q30656 azotobacter
27	7	2.8	217	16 Q9X5C4	Q9X5C4 streptococc
28	7	2.8	219	5 Q02210	Q02210 caenorhabdi
29	7	2.8	223	16 Q92R91	Q92R91 rhizobium m
30	7	2.8	231	10 Q94F39	Q94F39 arabidopsis
31	7	2.8	232	16 Q8ZKR6	Q8ZKR6 salmoneilla
32	7	2.8	232	16 Q8ZJM0	Q8ZJM0 yersinia pe
33	7	2.8	232	16 Q8Z2W2	Q8Z2W2 salmoneilla
34	7	2.8	234	16 Q8XIF6	Q8XIF6 clostridium
35	7	2.8	239	2 Q9X5C5	Q9X5C5 streptococc
36	7	2.8	244	6 Q9N0Q5	Q9N0Q5 philander m
37	7	2.8	255	16 Q8Z8J6	Q8Z8J6 salmoneilla
38	7	2.8	258	10 Q81480	Q81480 secale cere
39	7	2.8	259	17 Q974L3	Q974L3 sulfolobus
40	7	2.8	261	10 Q9LH16	Q9LH16 arabidopsis
41	7	2.8	265	16 Q07791	Q07791 mycobacteri
42	7	2.8	268	2 Q9X5C6	Q9X5C6 streptococc
43	7	2.8	287	5 Q20742	Q20742 caenorhabdi
44	7	2.8	289	16 Q9KNW7	Q9KNW7 vibrio chol
45	7	2.8	305	2 Q8VRY3	Q8VRY3 thermodesul
46	7	2.8	314	16 Q9A3Y3	Q9A3Y3 caulobacter
47	7	2.8	326	10 Q39108	Q39108 arabidopsis
48	7	2.8	326	10 Q9EPK0	Q9EPK0 arabidopsis
49	7	2.8	326	10 Q9SZM6	Q9SZM6 arabidopsis
50	7	2.8	331	10 Q9XEU4	Q9XEU4 oryza sativ
51	7	2.8	336	12 Q68405	Q68405 human cytom
52	7	2.8	349	10 Q9FLV7	Q9FLV7 arabidopsis
53	7	2.8	353	17 Q9HLQ5	Q9HLQ5 thermoplas
54	7	2.8	354	17 Q97C19	Q97C19 thermoplas
55	7	2.8	359	5 Q20880	Q20880 caenorhabdi
56	7	2.8	359	10 Q9LXR6	Q9LXR6 arabidopsis
57	7	2.8	360	2 Q68551	Q68551 pseudomonas
58	7	2.8	378	6 Q9NOR7	Q9NOR7 thylamys pa
59	7	2.8	379	6 Q9NOS0	Q9NOS0 gracillinanu
60	7	2.8	383	10 Q9LV20	Q9LV20 arabidopsis
61	7	2.8	385	6 Q9NOR9	Q9NOR9 gracillinanu
62	7	2.8	386	6 Q9MYN9	Q9MYN9 marmosops i
63	7	2.8	386	6 Q9MYN7	Q9MYN7 marmosops p
64	7	2.8	386	6 Q9MYM9	Q9MYM9 didelphis m
65	7	2.8	386	6 Q9MYM3	Q9MYM3 marmosops n
66	7	2.8	386	6 Q9NOS9	Q9NOS9 caluromysio
67	7	2.8	386	6 Q9NOS7	Q9NOS7 marmosops n
68	7	2.8	386	6 Q9NOS7	Q9NOS7 didelphis m
69	7	2.8	386	6 Q9NOS6	Q9NOS6 chironectes
70	7	2.8	386	6 Q9NOS5	Q9NOS5 marmosa lep
71	7	2.8	386	6 Q9NOS4	Q9NOS4 didelphis a
72	7	2.8	386	6 Q9NOS3	Q9NOS3 didelphis a
73	7	2.8	386	6 Q9NOS2	Q9NOS2 lutreolina
74	7	2.8	386	6 Q9NOR8	Q9NOR8 glirionia ve
75	7	2.8	386	6 Q9NOR6	Q9NOR6 caluromys i
76	7	2.8	386	6 Q9NOR5	Q9NOR5 micoureus d
77	7	2.8	386	6 Q9NOR4	Q9NOR4 monodelphis
78	7	2.8	386	6 Q9NOR3	Q9NOR3 micoureus d
79	7	2.8	386	6 Q9NOR2	Q9NOR2 monodelphis
80	7	2.8	386	6 Q9NOR1	Q9NOR1 philander m
81	7	2.8	386	6 Q9NOR0	Q9NOR0 marmosops n
82	7	2.8	386	6 Q9NOC9	Q9NOC9 marmosops n
83	7	2.8	386	6 Q9NOC8	Q9NOC8 metachirus
84	7	2.8	386	6 Q9NOC7	Q9NOC7 marmosops n
85	7	2.8	386	6 Q9NOC6	Q9NOC6 marmosa mur
86	7	2.8	386	6 Q9NOC4	Q9NOC4 metachirus
87	7	2.8	386	6 Q9NOC3	Q9NOC3 marmosa mur
88	7	2.8	386	6 Q9NOC2	Q9NOC2 lescodelphy
89	7	2.8	395	6 Q18857	Q18857 phascogale

90	7	2.8	397	5	Q9VLP7	Q9vlp7 drosophila
91	7	2.8	401	16	Q8X6P8	Q8x6p8 escherichia
92	7	2.8	401	16	Q99Q53	Q99q53 streptomyces
93	7	2.8	410	11	Q924S7	Q924s7 mus musculus
94	7	2.8	411	10	Q9FFX1	Q9ffx1 arabidopsis
95	7	2.8	412	13	Q91840	Q91840 xenopus lae
96	7	2.8	413	10	Q9M3V1	Q9m3v1 fagus sylv
97	7	2.8	415	6	O18856	O18856 caenolestes
98	7	2.8	419	13	Q8UUK1	Q8uuk1 gallus gall
99	7	2.8	421	16	Q8YGM8	Q8ygm8 bruceella me
100	7	2.8	437	16	Q99Z61	Q99z61 streptococc

ALIGNMENTS

RESULT 1
Q8RE60 PRELIMINARY; PRT; 202 AA.

Q8RE60; 01-JUN-2002 (TREMBlrel. 21, Created)
01-JUN-2002 (TREMBlrel. 21, Last sequence update)
01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Outer membrane protein.
GN FN1265.
OS Fusobacterium nucleatum (subsp. nucleatum).
OC Bacteria; Fusobacteria; Fusobacterium.
OX NCBI_TaxID=76856;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 25586;
RX MEDLINE=21886394; PubMed=11889109;
RA Kapatal V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
RA Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
RA Vasileva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,
RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
RA Fonstein M., Kyripides N., Overbeek R.;
RT "Genome sequence and analysis of the oral bacterium Fusobacterium
nucleatum strain ATCC 25586."
RL J. Bacteriol. 184:2005-2018(2002).
DR EMBL; AE010632; AAL95461.1; -.
KW Complete proteome.
SQ SEQUENCE 202 AA; 20749 MW; 8023AD9E0650B73F CRC64;

Query Match 3.2%; Score 8; DB 16; Length 202;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

36 GAALGAVA 43
|||||
Db 27 GAALGAVA 34

RESULT 2

Q94A26 PRELIMINARY; PRT; 223 AA.

Q94A26; 01-DEC-2001 (TREMBlrel. 19, Created)
01-DEC-2001 (TREMBlrel. 19, Last sequence update)
01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Atig74410/Fim20_9.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.

Shinn P., Chen H., Cheuk R., Kim C.J., Koeseema E., Meyers M.C.,
Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D.,
Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,
Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,

Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S.,
Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
"Arabidopsis cDNA clones."
RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

[2]
RP SEQUENCE FROM N.A.
RA Kim C.J., Chen H., Cheuk R., Meyers M.C., Shinn P., Banh J.,
RA Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis ORF clones."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AY050433; AAK91449.1; -.
DR EMBL; AY093797; AAM10413.1; -.
DR InterPro; IPR001841; ZnF_ring.
DR Pfam; PF00097; zf-C3HC4; 1.
KW Zinc-finger.
SQ SEQUENCE 223 AA; 24261 MW; 700187C970623CC0 CRC64;

Query Match 3.2%; Score 8; DB 10; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 GAALGAVA 43
|||||
Db 64 GAALGAVA 71

RESULT 3

Q8YS10 PRELIMINARY; PRT; 327 AA.

Q8YS10; 01-MAR-2002 (TREMBlrel. 20, Created)
01-MAR-2002 (TREMBlrel. 20, Last sequence update)
01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Hypothetical protein Alr3105.
GN ALR3105.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
cyanobacterium Anabaena sp. strain PCC 7120."
RL DNA Res. 8:205-213(2001).
DR EMBL; AP003591; BAB74804.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 327 AA; 38208 MW; 81558199DAF68B95 CRC64;

Query Match 3.2%; Score 8; DB 16; Length 327;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 QSSDALEA 93
|||||
Db 162 QSSDALEA 169

RESULT 4

Q8R6N2 PRELIMINARY; PRT; 577 AA.

AC Q8R6N2;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE ABC-type multidrug/protein/lipid transport system, ATPase
GN MDLB12 OR TTE2769.
OS Thermoaerobacter tengcongensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Thermoaerobacteriales; Thermoaerobacteriaceae; Thermoaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MB4T / JCM11007;
RX MEDLINE=21992816; PubMed=11997336;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
EMBL/ AE013214; AAM25873.1; -.
SQ COMPLETE proteome.
SQ SEQUENCE 577 AA; 66097 MW; BA6642DF1FBE7545 CRC64;
Query Match 3.2%; Score 8; DB 16; Length 577;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 224 ILSVIR 231
Db 160 ILSVIR 167
RESULT 5
Q9RU98 PRELIMINARY; PRT; 645 AA.
ID Q9RU98
AC Q9RU98;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE NADH dehydrogenase I, L subunit.
GN DRI494.
OS Deinococcus radiodurans.
OC Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R1;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Uitterback T., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
radiodurans R1.";
RL Science 286:1571-1577(1999).
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: TO NADH-UBIQUINONE/PLASTOQUINONE (COMPLEX I), VARIOUS
CHAINS.
CC -1- SIMILARITY: TO ONE OF THE POLYPEPTIDE CHAINS OF THE NADH-UBIQUINOL
OXIDOREDUCTASE OF CHLOROPLASTS OR MITOCHONDRIA.
EMBL/ AE001993; AAF11057.1; -.
DR TIGR; DRI494; -.
DR InterPro; IPR001750; Oxidored_q1.
DR InterPro; IPR001516; Oxidored_q1_N.
DR Pfam; PF00361; oxidored_q1; 1.
DR Pfam; PF00662; oxidored_q1_N; 1.
KW NAD; Oxidoreductase; Transmembrane; Complete proteome.

SQ SEQUENCE 645 AA; 69544 MW; AB5A3493F4DDE3F6 CRC64;
Query Match 3.2%; Score 8; DB 16; Length 645;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 212 VSAGVFHL 219
Db 345 VSAGVFHL 352
RESULT 6
P79805 PRELIMINARY; PRT; 773 AA.
ID P79805
AC P79805;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Microtubule-based motor protein.
GN FKIP2.
OS Morone saxatilis (Striped bass).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Moronidae; Morone.
OX NCBI_TaxID=34816;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=RETINA;
RA Bost-Ussinger L.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U64819; AAB39558.1; -.
DR HSSP; P17119; 3KAR.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR PROSITE; PS0067; KINESIN_MOTOR_DOMAIN2; 1.
KW ATP-binding; Coiled coil; Microtubules; Motor protein.
SQ SEQUENCE 773 AA; 87392 MW; B16832F0A4B0FA45 CRC64;
Query Match 3.2%; Score 8; DB 13; Length 773;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 57 SLRREVS 64
Db 62 SLRREVS 69
RESULT 7
Q84548 PRELIMINARY; PRT; 76 AA.
ID Q84548
AC Q84548;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE A228R protein.
GN A228R.
OS Paramesidium bursaria chlorella virus 1 (PBCV-1).
OC Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Chlorovirus.
OX NCBI_TaxID=10506;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=96187795; PubMed=8614977;
RX Lu Z., Li Y., Que Q., Kutish G.F., Rock D.L., Van Etten J.L.;
RT "Analysis of 94 kb of the chlorella virus PBCV-1 330-kb genome: map
positions 88 to 182.";
RL Virology 216:102-123(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20013326; PubMed=10544099;

RA Kaiser A., Vollmert M., Tholl D., Graves M.V., Gurnon J.R., King W.,
RA Lisee A.D., Nickerson K.W., Van Etten J.L.;
RT "Chlorella virus PBCV-1 encodes a functional homosperridine
RT synthase.";
RL Virology 263:254-262(1999).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20478054; PubMed=11021991;
RA Sun L., Gurnon J.R., Adams B.J., Graves M.V., Van Etten J.L.;
RT "Characterization of a beta-1,3-glucanase encoded by chlorella virus
RT PBCV-1.";
RL Virology 276:27-36(2000).
RN [4]
RP SEQUENCE FROM N.A.
RA Van Etten J.L.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Van Etten J.L.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA Van Etten J.L.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RA Graves M.V., Van Etten J.L.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE FROM N.A.
RA Graves M.V., Van Etten J.L.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [9]
RP SEQUENCE FROM N.A.
RA Gurnon J.R., Graves M.V., Van Etten J.L.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; U42580; AAC96596.1; --
SQ SEQUENCE 76 AA; 8736 MW; 36C1884955635134 CRC64;

Query Match 2.8%; Score 7; DB 12; Length 76;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 LSVLW 33
Db 69 LSVLW 75

RESULT 8
ID 096487 PRELIMINARY; PRT; 79 AA.
AC 096487;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Hypothetical 8.0 kDa protein (Fragment).
GN STEVOR 3D7REP-Z.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=W2;
RX MEDLINE=99094504; PubMed=9879895;
RA Cheng Q., Cloonan N., Fischer K., Thompson J., Waine G., Lanzer M.,
RA Saul A.;
RT "stevor and rif are Plasmodium falciparum multicopy gene families
RT which potentially encode variant antigens.";
RL Mol. Biochem. Parasitol. 97:161-176(1998).
DR EMBL; AF065197; AAD03647.1; --
DR InterPro; IPR002858; Rifin STEVOR.
DR Pfam; PF02009; Rifin STEVOR; 1.
KW Hypothetical protein.

FT NON_TER 1 1
FT NON_TER 79 79
SQ SEQUENCE 79 AA; 7981 MW; D17FF8DB0938F414 CRC64;

Query Match 2.8%; Score 7; DB 5; Length 79;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 AALGAVA 43
Db 17 AALGAVA 23

RESULT 9
ID 09NOA0 PRELIMINARY; PRT; 90 AA.
AC 09NOA0;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE unnamed protein product.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
RT libraries.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB046030; BAB01612.1; --
SQ SEQUENCE 90 AA; 9689 MW; 4F33636A3DF27274 CRC64;

Query Match 2.8%; Score 7; DB 6; Length 90;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 ALGAVAC 44
Db 67 ALGAVAC 73

RESULT 10
ID 09MFF2 PRELIMINARY; PRT; 106 AA.
AC 09MFF2;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE Orf106a protein.
GN ORF106A.
OS Beta vulgaris (Sugar beet).
OC Mitochondrion.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Beta.
OX NCBI_TaxID=3555;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TK81-O;
RX MEDLINE=20330382; PubMed=10871408;
RA Kubo T., Nishizawa S., Sugawara A., Itchoda N., Estiati A., Mikami T.;
RT "The complete nucleotide sequence of the mitochondrial genome of sugar
RT beet (Beta vulgaris L.) reveals a novel gene for tRNACys(GCA).";
RL Nucleic Acids Res. 28:2571-2576(2000).
DR EMBL; AP000396; BAA99290.1; --
KW Mitochondrion.
SQ SEQUENCE 106 AA; 11906 MW; 31B09126047F8602 CRC64;

Query Match 2.8%; Score 7; DB 8; Length 106;

Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 ASSPFL 9
|||||
Db 67 ASSPFL 73

RESULT 11

O91GK6 PRELIMINARY; PRT; 106 AA.

AC O91GK6; 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Type II envelope protein US9.
OS Pseudorabies virus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
NCBI_TaxID=10345;

SEQUENCE FROM N.A.

RA XIAO S.B., Fang L.R., Hong W.Z., Chen H.C.;

RT "Cloning and Expression of 11k gene of Pseudorabies Virus Strain Ea.";

RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF251220; AAF66961.1; -.

KW Envelope protein.

SQ SEQUENCE 106 AA; 11337 MW; .69FD0FEEB3529066 CRC64;

Query Match

Best Local Similarity 2.8%; Score 7; DB 12; Length 106;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 LLAPKGP 14
|||||
Db 30 LLAPKGP 36

RESULT 12

O9CQB7 PRELIMINARY; PRT; 122 AA.

AC O9CQB7; 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE 4930404J24RIK protein (2310004B22RIK protein) (RIKEN CDNA 2310004B22 gene).
4930404J24RIK OR 2310004B22RIK.

Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

RN [1]

SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=TESTIS, AND TONGUE;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaudo M.F.,

RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,

RA Guelincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,

RA Wyszaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).

RN [2]

RP SEQUENCE FROM N.A.

RA Strausberg R.;

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AK015083; BAB29706.1; -.

DR EMBL; AK009135; BAB26096.1; -.

DR EMBL; BC011339; AAH11339.1; -.

DR MGD; MGI:1921169; 4930404J24RIK.

DR MGD; MGI:1923685; 2310004B22RIK.

SQ SEQUENCE 122 AA; 14223 MW; A2E020FD0EA355E9 CRC64;

Query Match

Best Local Similarity 2.8%; Score 7; DB 11; Length 122;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 143 RRGRLQ 149
|||||
Db 95 RRGRLQ 101

RESULT 13

O23503 PRELIMINARY; PRT; 127 AA.

AC O23503;

DT 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE Hypothetical 14.6 kDa protein.

GN ZK470.3.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BRISTOL N2;

RX MEDLINE=99069613; PubMed=9851916;

RA None;

RT "Genome sequence of the nematode C. elegans: a platform for

RT investigating biology. The C. elegans Sequencing Consortium.";

RL Science 282:2012-2018(1998).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=BRISTOL N2;

RA Minx M.;

RT "The sequence of C. elegans cosmid ZK470.";

RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=BRISTOL N2;

RA Waterston R.;

RT "Direct Submission.";

RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; U39651; AAA80393.1; -.

KW Hypothetical protein.

SQ SEQUENCE 127 AA; 14574 MW; 0497D03C31D4E403 CRC64;

Query Match

Best Local Similarity 2.8%; Score 7; DB 5; Length 127;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 55 LOSLRE 61
|||||
Db 109 LOSLRE 115

RESULT 14

O94FP1 PRELIMINARY; PRT; 129 AA.

AC Q94FP1;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Succinate dehydrogenase subunit 3.
GN SDH3.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21347578; PubMed=11454775;
RA Adams K.L., Rosenbluth M., Qiu Y.L., Palmer J.D.;
RT "Multiple losses and transfers to the nucleus of two mitochondrial
RT succinate dehydrogenase genes during angiosperm evolution.";
RL Genetics 158:1289-1300(2001).
DR EMBL; AF362742; AAK73695.1; -.
InterPro; IPR000701; Sdh_cyt.
Pfam; PF01127; Sdh_cyt; I.
SEQUENCE 129 AA; 13863 MW; 761285BB6EA4B204 CRC64;

Query Match 2.8%; Score 7; DB 10; Length 129;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 36 GAALGAV 42
Db 107 GAALGAV 113

RESULT 15

O941A6 PRELIMINARY; PRT; 142 AA.
AC Q941A6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Atig08480/T27G7.10.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinn P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C.,
BA Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D.,
HA Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,
KA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
RA Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S.,
RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Arabidopsis cDNA clones.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,
BA Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
HA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
KA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis ORF clones.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY052314; AAK96507.1; -.
DR EMBL; AY061894; AAL31221.1; -.
SQ SEQUENCE 142 AA; 15813 MW; 011B5762B991D235 CRC64;

Query Match 2.8%; Score 7; DB 10; Length 142;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 36 GAALGAV 42
Db 74 GAALGAV 80

RESULT 16
O9S2C5 PRELIMINARY; PRT; 146 AA.
ID O9S2C5;
AC O9S2C5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical protein SCO0288.
GN SCO0288 OR SCF85.16.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycetales; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL110470; CAB54173.1; -.
KW Hypothetical protein.
SQ SEQUENCE 146 AA; 14974 MW; 4350BBBEF04315B6 CRC64;

Query Match 2.8%; Score 7; DB 16; Length 146;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 37 AALGAVA 43
Db 48 AALGAVA 54

RESULT 17
O9S6G3 PRELIMINARY; PRT; 156 AA.
ID O9S6G3;
AC O9S6G3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GRAB (Fragment).
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=API;
RX MEDLINE=99269061; PubMed=10336419;
RA Rasmussen M., Muller H.P., Bjorck L.;
RT "Protein GRAB of streptococcus pyogenes regulates proteolysis at the
RT bacterial surface by binding alpha2-macroglobulin.";
RL J. Biol. Chem. 274:15336-15344(1999).
DR EMBL; AF124400; AAD26339.1; -.
DR InterPro; IPR001899; Gram_pos_anchor.
DR PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.

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FT  NON_TER      1      1
FT  NON_TER      156     156
SQ  SEQUENCE      156 AA; 16587 MW; 19FAA98D0599D866 CRC64;

Query Match
Best Local Similarity 2.8%; Score 7; DB 2; Length 156;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  87 SSDALEA 93
    |||||
Db  58 SSDALEA 64

RESULT 18
Q9S6G4 PRELIMINARY; PRT; 156 AA.
ID  Q9S6G4
AC  Q9S6G4;
DT  01-MAY-2000 (TREMBlrel. 13, Created)
DT  01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT  01-DEC-2001 (TREMBlrel. 19, Last annotation update)
RT  GRAB (Fragment).
OC  Streptococcus pyogenes.
OC  Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC  Streptococcaceae; Streptococcus.
OX  NCBI_TaxID=1314;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=KT13;
RX  MEDLINE=99269061; Pubmed=10336419;
RA  Rasmussen M., Muller H.P., Bjorck L.;
RT  "Protein GRAB of streptococcus pyogenes regulates proteolysis at the
RT  bacterial surface by binding alpha2-macroglobulin.";
RL  J. Biol. Chem. 274:15336-15344(1999).
DR  EMBL; AF124401; AAD26340.1; -.
DR  InterPro; IPR001899; Gram_pos_anchor.
DR  PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
FT  NON_TER      1      1
FT  NON_TER      156     156
SQ  SEQUENCE      156 AA; 16575 MW; 0C20967E2FB0D866 CRC64;

Query Match
Best Local Similarity 2.8%; Score 7; DB 2; Length 156;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  87 SSDALEA 93
    |||||
Db  58 SSDALEA 64

SULT 19
Q9DAF5 PRELIMINARY; PRT; 170 AA.
ID  Q9DAF5
AC  Q9DAF5;
DT  01-JUN-2001 (TREMBlrel. 17, Created)
DT  01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT  01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE  170001IN12Rik protein.
GN  170001IN12RIK.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=C57BL/6J; TISSUE=TESTIS;
RX  MEDLINE=21085660; Pubmed=11217851;
RA  Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA  Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA  Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA  Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA  Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA  Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA  Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
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RA  Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA  Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA  Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA  Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA  Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA  Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA  Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA  Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA  Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA  Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsuki S.,
RA  Hayashizaki Y.;
RT  "Functional annotation of a full-length mouse cDNA collection.";
RL  Nature 409:685-690(2001).
DR  EMBL; AK005880; BAB24295.1; -.
DR  MGD; MGI:1916552; 170001IN12Rik.
DR  InterPro; IPR002965; P_rich_extensn.
DR  PRINTS; PR01217; PRICEXTENGN.
SQ  SEQUENCE      170 AA; 18852 MW; 4D4317B1A8A94581 CRC64;

Query Match
Best Local Similarity 2.8%; Score 7; DB 11; Length 170;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 PASSPFL 8
    |||||
Db  80 PASSPFL 86

RESULT 20
Q8ZWM1 PRELIMINARY; PRT; 175 AA.
ID  Q8ZWM1
AC  Q8ZWM1;
DT  01-MAR-2002 (TREMBlrel. 20, Created)
DT  01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT  01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE  P. aerophilum family 550 protein.
GN  PAE1719.
OS  Pyrobaculum aerophilum.
OC  Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC  Thermoproteaceae; Pyrobaculum.
OX  NCBI_TaxID=13773;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=IM2 / ATCC 51768 / DSM 7523;
RX  Pubmed=11792869;
RA  Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
RA  Miller J.H.;
RT  "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RT  aerophilum.";
RL  Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
DR  EMBL; AE009836; AAL63680.1; -.
KW  Complete proteome.
SQ  SEQUENCE      175 AA; 19680 MW; 8EDA0DD7474FBE85 CRC64;

Query Match
Best Local Similarity 2.8%; Score 7; DB 17; Length 175;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  25 PALSVAL 31
    |||||
Db  147 PALSVAL 153

RESULT 21
Q9RKN9 PRELIMINARY; PRT; 180 AA.
ID  Q9RKN9
AC  Q9RKN9;
DT  01-MAY-2000 (TREMBlrel. 13, Created)
DT  01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT  01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE  Putative membrane protein.
GN  SCO2289 OR SCC75A.35.
OS  Streptomyces coelicolor.
```

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxId=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL133220; CAB61735.1; -.
SEQUENCE 180 AA; 17710 MW; 57C052F39DAE0BDF CRC64;

Query Match

2.8%; Score 7; DB 16; Length 180;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 188 GROETLF 194
Db 173 GROETLF 179

RESULT 22

O9FSU6 PRELIMINARY; PRT; 183 AA.

AC O9FSU6;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Protein phosphatase 2C (PP2C) (Fragment).
GN PP2CF1.
OS Fagus sylvatica (Beechnut).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fagales; Fagaceae; Fagus.
OX NCBI_TaxId=28930;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SEED;
RA Lorenzo O.;
RA Thesis (2000), Fisiologia Vegetal, Facultad de Biologia,
RA Universidad de Salamanca.
DR EMBL; AJ298987; CAC09575.1; -.
DR HSSP; P35813; 1A6Q.
DR InterPro; IPR001932; PP2C-like.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2CC; 1.
FT SMART 1
FT NON_TER 183
FT NON_TER 183
SQ SEQUENCE 183 AA; 20365 MW; C9BA9F770EAEFFB0 CRC64;

Query Match 2.8%; Score 7; DB 10; Length 183;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 155 VRIQDAG 161
Db 120 VRIQDAG 126

RESULT 23

O8S7G3 PRELIMINARY; PRT; 185 AA.
ID . O8S7G3;
AC O8S7G3;
DT 01-JUN-2002 (TREMBLrel. 21, Created)

DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical 19.5 kDa protein.
GN OSJNB0048D20.11.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxId=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPONBARE;
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N.,
RA Gansberger K., Brenner M., Burgess S., Hance M., Shvartsbeyn M.,
RA Teitelin T., Riggs F., Hsiao J., Zisman V., Blunt S., Pai G.,
RA Vanaken S.E., Utterback T.R., Feldblyum T.V., Kalb E., Quackenbush J.,
RA Salzberg S.L., White O., Fraser C.M.;
RT "Oryza sativa chromosome 3 BAC OSJNB0048D20 genomic sequence.";
RT Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AC084766; AAL82525.1; -.
DR EMBL; AC084766; AAL82525.1; -.
KW Hypothetical protein.
SQ SEQUENCE 185 AA; 19508 MW; 7FF8D336DFE819FC CRC64;

Query Match

2.8%; Score 7; DB 10; Length 185;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 ASSPFL 9
Db 6 ASSPFL 12

RESULT 24

O9D5L5 PRELIMINARY; PRT; 192 AA.

AC O9D5L5;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE 4930424D10Rik protein.
GN 4930424D10Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TESTIS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Butt C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohatsu S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK015193; BAB29741.1; -.
DR MGD; MGI:1921026; 4930424D10Rik.
DR InterPro; IPR002965; P rich extensn.
DR PRINTS; PRO1217; PRICHEXTENSN.

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SQ SEQUENCE 192 AA; 20876 MW; 4CCA5438516F24E9 CRC64;
Query Match
Best Local Similarity 2.8%; Score 7; DB 11; Length 192;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 PASSPFL 8
   |||||
Db 80 PASSPFL 86

RESULT 25
Q9D9T6 PRELIMINARY; PRT; 193 AA.
AC Q9D9T6;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE 1700029H01RIK protein.
1700029H01RIK.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxId=10090;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TESTIS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaudo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald C., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL; AK006491; BAB24616.1; -
MGD; MGI:1917310; 1700029H01RIK.
DR InterPro; IPR002965; P rich extensn.
DR PRINTS; PR01217; PRICEXTENSN.
SQ SEQUENCE 193 AA; 20948 MW; 91332ECF952AE229 CRC64;

Query Match
Best Local Similarity 2.8%; Score 7; DB 11; Length 193;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 PASSPFL 8
   |||||
Db 80 PASSPFL 86

RESULT 26
Q30656 PRELIMINARY; PRT; 200 AA.
AC Q30656;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-JAN-1998 (TReMBLrel. 05, Last annotation update)
DE Hypothetical 22.5 kDa protein.
OS Azotobacter vinelandii.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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OC Azotobacter.
OX NCBI_TaxId=354;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TRANS;
RA Dean D.R.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF014048; AAB66329.1; -
KW Hypothetical protein.
SQ SEQUENCE 200 AA; 22517 MW; 608FEEDC5B8FAB0 CRC64;

Query Match
Best Local Similarity 2.8%; Score 7; DB 2; Length 200;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 SSPFLA 10
   |||||
Db 190 SSPFLA 196

RESULT 27
Q9X5C4 PRELIMINARY; PRT; 217 AA.
AC Q9X5C4;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE GRAB precursor (Protein GRAB) (Protein G-related alpha 2m-binding
DE protein).
GN GRAB OR SPY1357.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxId=1314;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=ATCC700294;
RA Rasmussen M., Muller H.P., Bjorck L.;
RT "Protein GRAB of Streptococcus pyogenes regulates proteolysis at the
RT bacterial surface by binding alpha2-macroglobulin.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / SEROTYPE M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.J., Meshan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren O., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL PROC. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
DR EMBL; AF124399; AAD26338.1; -
DR EMBL; AE006573; AAK34185.1; -
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR PRINTS; PR00015; GPOSANCHOR.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
KW Signal; Transmembrane; Complete proteome.
FT SIGNAL 1 33
FT CHAIN 34 217 GRAB.
FT CHAIN 34 217 GRAB.
SQ SEQUENCE 217 AA; 22836 MW; 79AAB8C4FF5F3FA06 CRC64;

Query Match
Best Local Similarity 2.8%; Score 7; DB 16; Length 217;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 87 SSDALEA 93
   |||||
Db 91 SSDALEA 97

RESULT 28
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002210
ID 002210 PRELIMINARY; PRT; 219 AA.
AC 002210;
DT 01-JUL-1997 (Tremblrel. 04, Created)
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE C01A2.6 protein.
GN C01A2.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Kershaw J.K.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
none;
"Genome sequence of the nematode C.elegans: A platform for
investigating biology.";
Science 282:2012-2018(1998).
DR EMBL; Z81029; CAB02701.1; -.
SQ SEQUENCE 219 AA; 25378 MW; E8C585E206275853 CRC64;

Query Match 2.8%; Score 7; DB 5; Length 219;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 LEAWENG 97
DB 85 LEAWENG 91

RESULT 29
Q92R91 PRELIMINARY; PRT; 223 AA.
AC Q92R91;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Probable transcription regulator protein.
GN FEUP OR R01014 OR SMC00458.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;
[1]
SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Bolstad P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
DR EMBL; AL591785; CAC45586.1; -.
DR InterPro; IPR001789; Response_reg.
DR InterPro; IPR003662; sub_transporter.
DR InterPro; IPR001867; Trans_reg_C.
DR Pfam; PF00072; response_reg; 1.
DR Pfam; PF00486; trans_reg_C; 1.
DR ProDom; PD000039; Response_reg; 1.
DR ProDom; PD000329; Trans_reg_C; 1.
DR PROSITE; PS00217; SUGAR_TRANSPORT_2; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 223 AA; 24786 MW; 8B4C7C1E34A74CF8 CRC64;

Query Match 2.8%; Score 7; DB 16; Length 223;

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Best Local Similarity 100.0%; Pred. No. 80;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 MGQVSR 184
DB 165 MGQVSR 171

RESULT 30
Q94F39 PRELIMINARY; PRT; 231 AA.
AC Q94F39;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE AT3g29575/MEB13_2.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Shin P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C.,
RA Tracy S.E., Banh J., Bowser L., Carninci P., Chung M.K.,
RA Goldsmith A.D., Hayashizaki Y., Ishida J., Jones T., Kamiya A.,
RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Pham P.K., Quach H.L.,
RA Sakano H., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C.,
RA Toriumi M., Yamada K., Yu G., Shinzaki K., Davis R.W., Theologis A.,
RA Becker J.R.;
RT "Arabidopsis cDNA clones.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF385741; AAK60331.1; -.
SQ SEQUENCE 231 AA; 25243 MW; 7CE5267AC501012D CRC64;

Query Match 2.8%; Score 7; DB 10; Length 231;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 ELQSLR 60
DB 74 ELQSLR 80

RESULT 31
Q8ZKR6 PRELIMINARY; PRT; 232 AA.
AC Q8ZKR6;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Response regulator in two-component regulatory system with CpxA,
DE regulates expression of protein folding and degrading factors (OmpR
DE family).
GN CPXR OR STM4059.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Lt2 / SGC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT Lt2.";
RL Nature 413:852-856(2001).
DR EMBL; AE008689; AAL22899.1; -.

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DR InterPro; IPR001789; Response_reg.
DR InterPro; IPR001867; Trans_reg_C.
DR Pfam; PF00072; response_reg; 1.
DR Pfam; PF00486; trans_reg_C; 1.
DR ProDom; PD000039; Response_reg; 1.
DR ProDom; PD000329; Trans_reg_C; 1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS50110; RESPONSE_REGULATORY; 1.
KW Complete proteome.
SQ SEQUENCE 232 AA; 26274 MW; 187C3AF5C59B44A CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 16; Length 232;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 GQVVSRE 185
DB 173 GQVVSRE 179

RESULT 32
ID Q8ZJM0 PRELIMINARY; PRT; 232 AA.
AC Q8ZJM0;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Two component system response regulatory protein.
GN CPXR OR YP000074.
OS Versinia pectis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Versinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / BIOVAR ORIENTALIS;
RX MEDLINE=21470413; PubMed=11586360;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Felwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT "Genome sequence of Versinia pectis, the causative agent of plague.";
RL Nature 413:523-527(2001).
DR EMBL; AL414141; CAC88940.1; -.
DR InterPro; IPR001789; Response_reg.
DR InterPro; IPR001867; Trans_reg_C.
DR Pfam; PF00072; response_reg; 1.
DR Pfam; PF00486; trans_reg_C; 1.
DR ProDom; PD000039; Response_reg; 1.
DR ProDom; PD000329; Trans_reg_C; 1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS50110; RESPONSE_REGULATORY; 1.
KW Complete proteome.
SQ SEQUENCE 232 AA; 26495 MW; 14AB928B080688A4 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 16; Length 232;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 GQVVSRE 185
DB 173 GQVVSRE 179

RESULT 33
ID Q8Z2W2 PRELIMINARY; PRT; 232 AA.
AC Q8Z2W2;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
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DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Two-component response regulatory protein.
GN STY3812.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
DR EMBL; AL627279; CAD09565.1; -.
DR InterPro; IPR001789; Response_reg.
DR InterPro; IPR001867; Trans_reg_C.
DR Pfam; PF00072; response_reg; 1.
DR Pfam; PF00486; trans_reg_C; 1.
DR ProDom; PD000039; Response_reg; 1.
DR ProDom; PD000329; Trans_reg_C; 1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS50110; RESPONSE_REGULATORY; 1.
KW Complete proteome.
SQ SEQUENCE 232 AA; 26301 MW; 975DF7F5D0887041 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 16; Length 232;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 GQVVSRE 185
DB 173 GQVVSRE 179

RESULT 34
ID Q8XIF6 PRELIMINARY; PRT; 234 AA.
AC Q8XIF6;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Probable glycoprotein endopeptidase.
GN CPE2165.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Clostridiales; Clostridiaceae; Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13 / TYPE A;
RX PubMed=11792842;
RA Shimizu T., Ohtani K., Hiraoka H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR EMBL; AP003193; BAB81871.1; -.
DR InterPro; IPR000905; Peptidase_M22.
DR ProDom; PD002367; Peptidase_M22; 1.
KW Complete proteome.
SQ SEQUENCE 234 AA; 25491 MW; CA01BF26760D2621 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 16; Length 234;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 112 KKHSHVL 118
|||||
Db 32 KKHSHVL 38

RESULT 35

Q9X5C5 PRELIMINARY; PRT; 239 AA.

AC Q9X5C5;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GRAB (Fragment).
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
[1]
SEQUENCE FROM N.A.

RX MEDLINE=99269061; PubMed=10336419;
RA Rasmussen M., Muller H.P., Bjorck L.;
RT "Protein GRAB of streptococcus pyogenes regulates proteolysis at the
bacterial surface by binding alpha2-macroglobulin."
RL J. Biol. Chem. 274:15336-15344(1999).
DR EMBL; AF124402; AAD26341.1; -.
DR InterPro; IPR001899; Gram_pos_anchor.
DR PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
FT NON_TER 1 239
SQ SEQUENCE 239 AA; 24846 MW; 61AC4F6F863AF0F5 CRC64;

Query Match 2.8%; Score 7; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 SSDALEA 93
|||||
Db 58 SSDALEA 64

RESULT 36

Q9N0Q5 PRELIMINARY; PRT; 244 AA.

AC Q9N0Q5;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Interphotoreceptor retinoid binding protein (Fragment).
GN IRBP.
OS Philander mcilhennyi.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Philander.
OX NCBI_TaxID=42729;
[1]

RP SEQUENCE FROM N.A.
RA Jansa S.A., Voss R.S.;
RT "Phylogenetic studies on didelphid marsupials I. Introduction and
preliminary results from nuclear IRBP gene sequences."
RL J. Mammal. Evol. 7:43-77(2000).
DR EMBL; AF257706; AAF72033.1; -.
DR InterPro; IPR003581; TSpc.
DR Pfam; PF02692; IRBP; 1.
DR SMART; SM00245; TSpc; 1.
KW Receptor.

FT NON_TER 1 1
FT NON_TER 244 244
SQ SEQUENCE 244 AA; 26802 MW; 0948A8E3979E0EB5 CRC64;

Query Match 2.8%; Score 7; DB 6; Length 244;
Best Local Similarity 100.0%; Pred. No. 87;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 219 LHOGDIL 225
|||||
Db 141 LHOGDIL 147

RESULT 37

Q8Z8J6 PRELIMINARY; PRT; 255 AA.

AC Q8Z8J6;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Molybdopterin-containing oxidoreductase membrane anchor subunit.
GN STY0661.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=601;
[1]
SEQUENCE FROM N.A.

RP STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltham T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagsels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Garra P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrall B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
enterica serovar Typhi CT18."
RL Nature 413:848-852(2001).
DR EMBL; AL627267; CAD05090.1; -.
KW Complete proteome.
SQ SEQUENCE 255 AA; 27606 MW; CCD602E40097FC5A CRC64;

Query Match 2.8%; Score 7; DB 16; Length 255;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 203 HPDRAYN 209
|||||
Db 61 HPDRAYN 67

RESULT 38

Q81480 PRELIMINARY; PRT; 258 AA.

AC Q81480;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Thioredoxin peroxidase.
GN TPX1.

OS Secale cereale (Rye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Secale.
OX NCBI_TaxID=4550;
[1]

RP SEQUENCE FROM N.A.
RX MEDLINE=99056866; PubMed=9867602;
RA Berberich T., Uebeler M., Feterabend J.;
RT "Cloning of a cDNA encoding a Thioredoxin Peroxidase Homolog from
Winter Rye (Accession No. AF076920) (PGR98-167)."
RL Plant Physiol. 118:711-711(1998).
DR EMBL; AF076920; AAC78473.1; -.
DR HSSP; P30041; IPRX.
DR InterPro; IPR000866; Ahpc-TSA.
DR Pfam; PF00578; Ahpc-TSA; 1.

KW Peroxidase.
SQ SEQUENCE 258 AA; 28133 MW; 9C3BD415FE8DA9A8 CRC64;

Query Match 2.8%; Score 7; DB 10; Length 258;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 140 PALRRGR 146
|||||
Db 32 PALRRGR 38

RESULT 39

Q974L3 PRELIMINARY; PRT; 259 AA.
AC Q974L3;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
Putative pyrroline-5-carboxylate reductase.
ST0646.
Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=111955;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JCM 10545 / 7;
RX PubMed=11572479;
RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Ankal A., Kosugi H., Hosoyama A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagi M., Nishimura M., Yamagishi A.,
RA Oshima T., Kikuchi H.;
RT "Complete genome sequence of an aerobic thermoacidophilic
RT Crenarchaeon, Sulfolobus tokodaii strain7.";
RL DNA Res. 8:123-140(2001).
DR EMBL; AP000983; BAB55645.1; -.
DR InterPro; IPR000304; P5CR.
DR Pfam; PF01089; P5CR; 1.
DR PROSITE; PS00521; P5CR; UNKNOWN 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 259 AA; 28476 MW; 3A9614D4A6BBF936 CRC64;

Query Match 2.8%; Score 7; DB 17; Length 259;
Best Local Similarity 100.0%; Pred. No. 92;
atches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

38 ALGAVAC 44
|||||
Db 172 ALGAVAC 178

RESULT 40

Q9LH16 PRELIMINARY; PRT; 261 AA.
AC Q9LH16;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE Similarity to unknown protein.
OS Arabidopsis thaliana (mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Nakamura Y.;
RT "Structural Analysis of Arabidopsis thaliana Chromosome 3. III.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AP002457; BAB01982.1; -.
SQ SEQUENCE 261 AA; 28447 MW; 0F7715A05B45367D CRC64;

Query Match 2.8%; Score 7; DB 10; Length 261;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 ELOSLR 60
|||||
Db 74 ELOSLR 80

RESULT 41

O07791 PRELIMINARY; PRT; 265 AA.
AC O07791;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical protein RV0587.
GN RV0587 OR MTCY19H5.35C OR MT0616.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Broesch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sultston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).

RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / OSHKOSH;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; Z97182; CAB09951.1; -.
DR EMBL; AE006958; AAK44840.1; -.
DR TIGR; MT0616; -.
DR TubercuList; RV0587; -.
DR InterPro; IPR003453; DUF140.
DR Pfam; PF02405; DUF140; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 265 AA; 27327 MW; 1632EE79C5D0CD44 CRC64;

Query Match 2.8%; Score 7; DB 16; Length 265;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 GALGAV 42
|||||
Db 92 GALGAV 98

RESULT 42
Q9X5C6 PRELIMINARY; PRT; 268 AA.
ID Q9X5C6
AC Q9X5C6;

DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE GRAB (Fragment).
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AP49;
RX MEDLINE=99269061; PubMed=10336419;
RA Rasmussen M., Muller H.P., Bjorck L.;
RT "Protein GRAB of streptococcus pyogenes regulates proteolysis at the
bacterial surface by binding alpha2-macroglobulin."
RL J. Biol. Chem. 274:15336-15344(1999).
DR EMBL; AF124403; AAD26342.1; -.
DR InterPro; IPR001899; Gram_pos_anchor.
DR PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
NON_TER 1 1
SEQUENCE 268 AA; 27744 MW; 1C59239260CDCE7 CRC64;
Query Match 2.8%; Score 7; DB 2; Length 268;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 87 SSDALEA 93
Db 58 SSDALEA 64
RESULT 43
Q20742
ID Q20742 PRELIMINARY; PRT; 287 AA.
AC Q20742;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE F54B11.7 protein.
GN F54B11.7.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Swinburne J.;
RT Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
KP [2]
KP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; Z70208; CAA94139.1; -.
SQ SEQUENCE 287 AA; 31590 MW; 1E6EC2894784A3C4 CRC64;
Query Match 2.8%; Score 7; DB 5; Length 287;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 129 DSDVTE 135
Db 52 DSDVTE 58
RESULT 44
ID Q9KNW7 PRELIMINARY; PRT; 289 AA.
AC Q9KNW7;
DT 01-OCT-2000 (TReMBLrel. 15, Created)

DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Phosphoribulokinase.
GN VC2613.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EL TOR N16961 / SEROTYPE O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
cholerae."
RL Nature 406:477-483(2000).
DR EMBL; AE004328; AAF95754.1; -.
DR HSSP; P12033; 1A7J.
DR TIGR; VC2613; -.
DR InterPro; IPR001324; PRK.
DR Pfam; PF00485; PRK.1.
DR PRINTS; PR00478; PHRIBLKINASE.
KW Kinase; Complete proteome.
SQ SEQUENCE 289 AA; 32785 MW; 219167FC5C61E181 CRC64;

Query Match 2.8%; Score 7; DB 16; Length 289;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 PWQSLPE 85
Db 116 PWQSLPE 122

RESULT 45
Q8VRV3
ID Q8VRV3 PRELIMINARY; PRT; 305 AA.
AC Q8VRV3;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Adenosine-5'-phosphosulfate reductase alpha subunit (Fragment).
GN APSA.
OS Thermodesulfobivrio islandicus.
OC Bacteria; Nitrospirae; Nitrospirales; Nitrospiraceae;
OC Thermodesulfobivrio.
OX NCBI_TaxID=53423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 12570;
RX MEDLINE=21617390; PubMed=11741869;
RA Friedrich M.W.;
RT "Phylogenetic Analysis Reveals Multiple Lateral Transfers of
Adenosine-5'-Phosphosulfate Reductase Genes among Sulfate-Reducing
Microorganisms."
RL J. Bacteriol. 184:278-289(2002).
DR EMBL; AF418113; AAL57380.1; -.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 305 AA; 34078 MW; DEB25675D4E24816 CRC64;

Query Match 2.8%; Score 7; DB 2; Length 305;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 SREGGR 189
Db 171 SREGGR 177

RESULT 46
Q9A3Y3 PRELIMINARY; PRT; 314 AA.
AC Q9A3Y3; 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE Peptidyl-prolyl cis-trans isomerase family protein.
GN CC3067.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
OC Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B., DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Uterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O., Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RA "Complete genome sequence of Caulobacter crescentus.";
RT Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
RL EMBL; AE005970; AAK25029.1; -.
DR TIGR; CC3067; -.
DR InterPro; IPR000297; Rotamase.
DR Pfam; PF00639; Rotamase; 1.
DR PROSITE; PS01096; PPIC_PPIASE_1; UNKNOWN_1.
DR PROSITE; PS50198; PPIC_PPIASE_2; 1.
KM Isomerase; Complete proteome.
SQ SEQUENCE 314 AA; 33652 MW; B7A9289B5D3523AB CRC64;
Query Match 2.8%; Score 7; DB 16; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 39 LGAVACA 45
Db 4 LGAVACA 10
RESULT 47
Q39108 PRELIMINARY; PRT; 326 AA.
Q39108;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Geranylgeranyl pyrophosphate synthase-related protein precursor.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OC NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA "Nucleotide sequence of a putative geranylgeranyl pyrophosphate synthase (GenBank L40577) from Arabidopsis (PGR95-018).";
RT Plant Physiol. 108:1343-1343(1995).
RL EMBL; L40577; AAA81879.1; -.
DR InterPro; IPR000092; Polyprenyl_synth.
DR Pfam; PF00348; polyprenyl_synth; 1.
DR PROSITE; PS00723; POLYPRENYL_SYNTHET_1; 1.
KW Transit peptide.
FT TRANSIT 1 47 POTENTIAL.
FT CHAIN 48 326 GERANYLGERANYL PYROPHOSPHATE SYNTHASE-

FT SEQUENCE 326 AA; 35240 MW; FF9224BCC2D7B570 CRC64;
SQ RELATED PROTEIN.
Query Match 2.8%; Score 7; DB 10; Length 326;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 54 ELQSLR 60
Db 242 ELQSLR 248
RESULT 48
Q9FPK0 PRELIMINARY; PRT; 326 AA.
AC Q9FPK0;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE AT4G38460.
GN AT4G38460/F20M13.20.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OC NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinn P., Chen H., Cheuk R., Kim C.J., Banh J., Bowser L., Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M., Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M., Seki M., Southwick A., Tortum M., Yamada K., Yu G., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RA "Arabidopsis cDNA clones.";
RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF324662; AAG40013.1; -.
DR InterPro; IPR000092; Polyprenyl_synth.
DR Pfam; PF00348; polyprenyl_synth; 1.
DR PROSITE; PS00723; POLYPRENYL_SYNTHET_1; 1.
SQ SEQUENCE 326 AA; 35246 MW; 894C5A00740CD475 CRC64;
Query Match 2.8%; Score 7; DB 10; Length 326;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 54 ELQSLR 60
Db 242 ELQSLR 248
RESULT 49
Q9SZM6 PRELIMINARY; PRT; 326 AA.
AC Q9SZM6;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Geranylgeranyl pyrophosphate synthase-related protein (AT4G38460/F20M13.20).
GN F20M13.20 OR AT4G38460.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OC NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Wedler H., Kutzner M., Wandt R., Bancroft I., Mewes H.W., Mayer K.F.X., Scheller C.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [2]

RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Wedler H., Kutzner M., Wambutt R., Mewes H.W., Lemcke K.,
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Liu S.X., Sakano H., Pham P.K., Yamada K., Banh J., Etgu P., Lee J.M.,
RA Toriumi M., Yu G., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "Full Length cDNA of gene F20M13 20/AT4g38460 (GI:7270829).";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Full Length cDNA of gene F20M13 20/AT4g38460 (GI:7270829).";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RA Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis ORF clones.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Meyers M.C., Shinn P., Banh J.,
RA Bowser L., Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
RA Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M.,
RA Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M.,
RA Seki M., Southwick A., Toriumi M., Yamada K., Yu G., Shinozaki K.,
RA Davis R.W., Theologis A., Ecker J.R.;
RT "Arabidopsis cDNA clones.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [9]
RP SEQUENCE FROM N.A.
RA EMBL; AL035540; CAB37502.1; -;
DR EMBL; AL161593; CAB80510.1; -;
DR EMBL; AF326906; AAG41488.1; -;
DR EMBL; AF339725; AAK00407.1; -;
DR EMBL; AY057734; AAL15364.1; -;
DR EMBL; AF372915; AAK49631.1; -;
DR InterPro; IPR000092; Polyprenyl synth.
DR Pfam; PF00348; polyprenyl synth.1.
DR PROSITE; PS00723; POLYPRENYL SYNTHET 1; 1.
SQ SEQUENCE 326 AA; 35188 MW; 89494E00740CD475 CRC64;

Query Match 2.8%; Score 7; DB 10; Length 326;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 54 ELQSLR 60
Db 242 ELQSLR 248

RESULT 50

O9XEU4
ID O9XEU4 PRELIMINARY; PRT; 331 AA.
AC O9XEU4;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE Putative reverse transcriptase.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Llaca V., Lou A., Young S., Messing J.;
RT "Microsytiny in a gene-dense region in maize, sorghum, and rice.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF119222; AAD27672.1; -;
KW RNA-directed DNA polymerase.
SQ SEQUENCE 331 AA; 37867 MW; BA451072D5D8BD0C CRC64;

Query Match 2.8%; Score 7; DB 10; Length 331;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 52 QTELOSL 58
Db 121 QTELOSL 127

RESULT 51
O68405
ID O68405 PRELIMINARY; PRT; 336 AA.
AC O68405;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE Orf UL151.
OS Human cytomegalovirus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Cytomegalovirus.
OX NCBI_TaxID=10359;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TOLEDO;
RX MEDLINE=96099416; PubMed=8523595;
RA Cha T.A., Tom E., Kemble G.W., Duke G.M., Mocarski E.S., Spaete R.R.;
RT "Human cytomegalovirus clinical isolates carry at least 19 genes not
found in laboratory strains."
RL J. Virol. 70:78-83(1996).
DR EMBL; U33331; AAA85892.1; -;
SQ SEQUENCE 336 AA; 35116 MW; 9F865E5019F69D0C CRC64;

Query Match 2.8%; Score 7; DB 12; Length 336;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 142 LRRGRGL 148
Db 82 LRRGRGL 88

RESULT 52
O9FLV7
ID O9FLV7 PRELIMINARY; PRT; 349 AA.
AC O9FLV7;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE Genomic DNA, chromosome 5, p1 clone:MZF18.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eucroside II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=98290546; PubMed=9628582;
RA Sato S., Kaneko T., Kotani H., Nakamura Y., Asamizu E., Miyajima N.,
RA Tabata S.:
RT "Structural analysis of Arabidopsis thaliana chromosome 5. IV.
RT Sequence features of the regions of 1,456,315 bp covered by nineteen
RT physically assigned pl and TAC clones."
RL DNA Res. 5:41-54(1998).
DR EMBL; AB009056; BAB08728.1;
SQ SEQUENCE 349 AA; 39783 MW; 33F598698FB41CC9 CRC64;

Query Match 2.8%; Score 7; DB 10; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 53
Q9HLO5 PRELIMINARY; PRT; 353 AA.
AC Q9HLO5;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Hemin permease (hemu) related protein.
GN TA0172.
OS Thermoplasma acidophilum.
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC Thermoplasmataceae; Thermoplasma.
OX NCBI_TaxID=2303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 1728;
RX MEDLINE=20479972; PubMed=11029001;
RA Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
RA Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.:
RT "The genome sequence of the thermoacidophilic scavenger Thermoplasma
RT acidophilum."
RL Nature 407:508-513(2000).
DR EMBL; AL445063; CAC11318.1;
DR InterPro; IPR000522; FeccD.
PFam; PF01032; FeccD; 1.
ProDom; PD001557; FeccD; 1.
KW Complete proteome.
SQ SEQUENCE 353 AA; 37885 MW; 1D04DC507D2DA4EC CRC64;

Query Match 2.8%; Score 7; DB 17; Length 353;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 GAALGAV 42
DB 116 GAALGAV 122

RESULT 54
Q97C19 PRELIMINARY; PRT; 354 AA.
AC Q97C19;
DT 01-OCT-2001 (TReMBLrel. 18, Created)
DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Iron III diclitate transport system permease protein.
GN TV0286 OR TVG0296872.
OS Thermoplasma volcanium.
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;

OC Thermoplasmataceae; Thermoplasma.
OX NCBI_TaxID=50339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GSS1 / DSM 4299 / JCM 9571;
RX MEDLINE=20570466; PubMed=11121031;
RA Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,
RA Kawashima-Chya Y., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T.,
RA Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.:
RT "Archaeal adaptation to higher temperatures revealed by genomic
RT sequence of Thermoplasma volcanium."
RL Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
DR EMBL; AP000991; BAB59428.1;
DR InterPro; IPR000522; FeccD.
DR Pfam; PF01032; FeccD; 1.
DR ProDom; PD001557; FeccD; 1.
KW Complete proteome.
SQ SEQUENCE 354 AA; 38220 MW; 5347A99FFDB3D588 CRC64;

Query Match 2.8%; Score 7; DB 17; Length 354;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 GAALGAV 42
DB 117 GAALGAV 123

RESULT 55
Q20880 PRELIMINARY; PRT; 359 AA.
ID Q20880;
AC Q20880;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE F56D5.1 protein.
GN F56D5.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Matthews P.:
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; Z69662; CAA93499.1;
DR InterPro; IPR000087; Collagen.
DR InterPro; IPR002486; Col cuticle_N.
DR Pfam; PF01391; Collagen_2.
DR Pfam; PF01484; Col cuticle_N; 1.
SQ SEQUENCE 359 AA; 36515 MW; 1F66C351DC24770D CRC64;

Query Match 2.8%; Score 7; DB 5; Length 359;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PKGPPGN 17
DB 221 PKGPPGN 227

RESULT 56
Q9LRX6 PRELIMINARY; PRT; 359 AA.
ID Q9LRX6;
AC Q9LRX6;
DT 01-OCT-2000 (TReMBLrel. 15, Created)

DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE Similarity to HETI protein from Anabaena PCC7120.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eukosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=20277480; PubMed=10819329;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
features of the regions of 4,504,864 bp covered by sixty P1 and TAC
clones."
DNA Ref. 7:131-135 (2000).
DR EMBL: AB028609; BAB02895.1; -
SQ SEQUENCE 359 AA; 40668 MW; C6042D19BBBF3FD CRC64;

Query Match 2.8%; Score 7; DB 10; Length 359;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 100 SRKRRV 106
Db 179 SRKRRV 185

RESULT 57

ID 068551 PRELIMINARY; PRT; 360 AA.
AC 068551;
DT 01-AUG-1998 (TReMBLrel. 07, Created)
DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Triacylglycerol lipase (EC 3.1.1.3).
OS Pseudomonas luteola.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=47886;
RN [1]
RP SEQUENCE FROM N.A.
RA Litchauer D., Ginster A., Skein E.;
RT Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
EMBL: AF050153; AAC05510.1; -
DR HSSP; P22088; 3LP.
DR InterPro; IPR000073; Abhydrolase.
DR InterPro; IPR000734; Lipase.
DR InterPro; IPR000379; Set_estrs_site.
DR Pfam; PF00561; abhydrolase; 1.
DR PROSITE; PS00120; LIPASE_SER; 1.
KW Hydrolase.
SQ SEQUENCE 360 AA; 37189 MW; BD8080C22D58AFB0 CRC64;

Query Match 2.8%; Score 7; DB 2; Length 360;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 40 GAVACAM 46
Db 8 GAVACAM 14

RESULT 58

ID 09N0R7 PRELIMINARY; PRT; 378 AA.
AC 09N0R7;

DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE Interphotoreceptor retinoid binding protein (Fragment).
GN IRBP.
OS Thylamys pallidior (pallid fat-tailed opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Thylamys.
OX NCBI_TaxID=126301;
RN [1]
RP SEQUENCE FROM N.A.
RA Jansa S.A., Voss R.S.;
RT "Phylogenetic studies on didelphid marsupials I. Introduction and
preliminary results from nuclear IRBP gene sequences."
RL J. Mammal. Evol. 7:43-77 (2000).
DR EMBL: AF257689; AAF72016.1; -
DR InterPro; IPR003581; TSpc.
DR Pfam; PF02692; IRBP; 1.
DR SMART; SM00245; TSpc; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 378 AA; 41175 MW; 3BE299E78D586558 CRC64;

Query Match 2.8%; Score 7; DB 6; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 219 LHQGDIL 225
Db 133 LHQGDIL 139

RESULT 59

ID 09N0S0 PRELIMINARY; PRT; 379 AA.
AC 09N0S0;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE Interphotoreceptor retinoid binding protein (Fragment).
GN IRBP.
OS Gracillanus microtarsus (Brazilian gracile mouse opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Gracillanus.
OX NCBI_TaxID=126289;
RN [1]
RP SEQUENCE FROM N.A.
RA Jansa S.A., Voss R.S.;
RT "Phylogenetic studies on didelphid marsupials I. Introduction and
preliminary results from nuclear IRBP gene sequences."
RL J. Mammal. Evol. 7:43-77 (2000).
DR EMBL: AF257686; AAF72013.1; -
DR InterPro; IPR003581; TSpc.
DR Pfam; PF02692; IRBP; 1.
DR SMART; SM00245; TSpc; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 379 AA; 41197 MW; C6A8B0248D068FB0 CRC64;

Query Match 2.8%; Score 7; DB 6; Length 379;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 219 LHQGDIL 225
Db 134 LHQGDIL 140

RESULT 60

ID 09LV20 PRELIMINARY; PRT; 383 AA.
AC 09LV20

AC Q9LV20;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Nodulin-like protein.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=20363099; PubMed=10907853;
NA Nakamura Y.;
NA "Structural analysis of Arabidopsis thaliana chromosome 3. II.
NA Sequence features of the regions of 4,251,695 bp covered by ninety pl,
NA TAC and BAC clones."
RL DNA Res. 7:217-221(2000).
DR EMBL; AB020749; BAB02033.1; -
DR InterPro; IPR000620; DUF6.
DR Pfam; PF00892; DUF6; 2.
KW SMART; SM00245; TSpc; 1.
SQ SEQUENCE 383 AA; 42845 MW; E014B3128B3FB517 CRC64;
FT NON_TER 1
FT NON_TER 385
SQ SEQUENCE 385 AA; 41973 MW; E2C0E0A4E7B05322 CRC64;
Query Match 2.8%; Score 7; DB 6; Length 385;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 219 LHQGDIL 225
DB 140 LHQGDIL 146

RESULT 62
Q9MYN9 PRELIMINARY; PRT; 386 AA.
AC Q9MYN9;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Interphotoreceptor retinoid binding protein (Fragment).
GN IRBP.
OS Marmosops impavidus (Andean slender mouse opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Marmosops.
OX NCBI_TaxID=42722;
RN [1]
RP SEQUENCE FROM N.A.
RA Jansa S.A., Voss R.S.;
RT "Phylogenetic studies on didelphid marsupials I. Introduction and
RT preliminary results from nuclear IRBP gene sequences."
RL J. Mammal. Evol. 7:43-77(2000).
DR EMBL; AF257695; AAF72022.1; -
DR EMBL; AF257698; AAF72025.1; -
DR InterPro; IPR003581; TSpc.
DR Pfam; PF02692; IRBP; 1.
DR SMART; SM00245; TSpc; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 386
SQ SEQUENCE 386 AA; 42147 MW; 316E9530868EA4E3 CRC64;
Query Match 2.8%; Score 7; DB 6; Length 386;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 219 LHQGDIL 225
DB 141 LHQGDIL 147

RESULT 63
Q9MYN7 PRELIMINARY; PRT; 386 AA.
AC Q9MYN7;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Interphotoreceptor retinoid binding protein (Fragment).
GN IRBP.
OS Marmosops parvidens (delicate slender mouse opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Marmosops.
OX NCBI_TaxID=126298;
RN [1]
RP SEQUENCE FROM N.A.
RA Jansa S.A., Voss R.S.;
RT "Phylogenetic studies on didelphid marsupials I. Introduction and
RT preliminary results from nuclear IRBP gene sequences."
RL J. Mammal. Evol. 7:43-77(2000).
DR EMBL; AF257680; AAF72007.1; -
DR EMBL; AF257677; AAF72004.1; -
DR InterPro; IPR003581; TSpc.
DR Pfam; PF02692; IRBP; 1.
DR SMART; SM00245; TSpc; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 386
SQ SEQUENCE 386 AA; 42087 MW; 3530F20B3A0D96DB CRC64;
Query Match 2.8%; Score 7; DB 6; Length 386;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 219 LHQGDIL 225
|||||
Db 141 LHQGDIL 147

RESULT 64

Q9MYM9

ID Q9MYM9 PRELIMINARY; PRT; 386 AA.

AC Q9MYM9; 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Interphotoreceptor retinoid binding protein (Fragment).
GN IRBP.
OS Didelphis marsupialis (Southern opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX NCBI_TaxID=9268;
RN [1]
RP SEQUENCE FROM N.A.

RA Jansa S.A., Voss R.S.;
RT "Phylogenetic studies on didelphid marsupials I. Introduction and preliminary results from nuclear IRBP gene sequences.";
RL J. Mammal. Evol. 7:43-77(2000).

DR EMBL; AF257708; AAF72035.1; -.
DR EMBL; AF257703; AAF72030.1; -.
DR InterPro; IPR003581; TSPC.
DR Pfam; PF02692; IRBP; 1.
DR SMART; SM00245; TSPC; 1.

KW Receptor.
FT NON_TER 1 1
FT NON_TER 386 386

SO SEQUENCE 386 AA; 42086 MW; 70EDFF445D9AAB69 CRC64;

Query Match

Best Local Similarity 2.8%; Score 7; DB 6; Length 386;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 219 LHQGDIL 225
|||||
Db 141 LHQGDIL 147

RESULT 65

Q9MYM3

ID Q9MYM3 PRELIMINARY; PRT; 386 AA.

AC Q9MYM3; 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Interphotoreceptor retinoid binding protein (Fragment).
GN IRBP.

OS Marmosops noctivagus (white-bellied slender mouse opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Marmosops.
OX NCBI_TaxID=126296;
RN [1]
RP SEQUENCE FROM N.A.

RA Jansa S.A., Voss R.S.;
RT "Phylogenetic studies on didelphid marsupials I. Introduction and preliminary results from nuclear IRBP gene sequences.";
RL J. Mammal. Evol. 7:43-77(2000).

DR EMBL; AF257704; AAF72031.1; -.
DR EMBL; AF257696; AAF72023.1; -.
DR InterPro; IPR003581; TSPC.
DR Pfam; PF02692; IRBP; 1.
DR SMART; SM00245; TSPC; 1.

KW Receptor.
FT NON_TER 1 1
FT NON_TER 386 386

SO SEQUENCE 386 AA; 42061 MW; C14C953095369F70 CRC64;

Query Match

2.8%; Score 7; DB 6; Length 386;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 219 LHQGDIL 225
|||||
Db 141 LHQGDIL 147

RESULT 66

Q9NOS9

ID Q9NOS9 PRELIMINARY; PRT; 386 AA.

AC Q9NOS9; 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Interphotoreceptor retinoid binding protein (Fragment).
GN IRBP.
OS Caluromyslops irrupta (black-shouldered opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Caluromyslops.
OX NCBI_TaxID=126286;
RN [1]
RP SEQUENCE FROM N.A.

RA Jansa S.A., Voss R.S.;
RT "Phylogenetic studies on didelphid marsupials I. Introduction and preliminary results from nuclear IRBP gene sequences.";
RL J. Mammal. Evol. 7:43-77(2000).

DR EMBL; AF257675; AAF72002.1; -.
DR InterPro; IPR003581; TSPC.
DR Pfam; PF02692; IRBP; 1.
DR SMART; SM00245; TSPC; 1.

KW Receptor.
FT NON_TER 1 1
FT NON_TER 386 386

SO SEQUENCE 386 AA; 42106 MW; BF2B256F970FC1AC CRC64;

Query Match

Best Local Similarity 2.8%; Score 7; DB 6; Length 386;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 219 LHQGDIL 225
|||||
Db 141 LHQGDIL 147

RESULT 67

Q9NOS8

ID Q9NOS8 PRELIMINARY; PRT; 386 AA.

AC Q9NOS8; 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Interphotoreceptor retinoid binding protein (Fragment).
GN IRBP.

OS Marmosops noctivagus (white-bellied slender mouse opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Marmosops.
OX NCBI_TaxID=126296;
RN [1]
RP SEQUENCE FROM N.A.

RA Jansa S.A., Voss R.S.;
RT "Phylogenetic studies on didelphid marsupials I. Introduction and preliminary results from nuclear IRBP gene sequences.";
RL J. Mammal. Evol. 7:43-77(2000).

DR EMBL; AF257676; AAF72003.1; -.
DR InterPro; IPR003581; TSPC.
DR Pfam; PF02692; IRBP; 1.
DR SMART; SM00245; TSPC; 1.

KW Receptor.
FT NON_TER 1 1
FT NON_TER 386 386

SO SEQUENCE 386 AA; 42008 MW; 351DC4758E37346A CRC64;

Query Match 2.8%; Score 7; DB 6; Length 386;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 219 LHOGDIL 225
Db 141 LHOGDIL 147

RESULT 68

Q9NOS7 PRELIMINARY; PRT; 386 AA.
ID Q9NOS7
AC Q9NOS7;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE Interphotoreceptor retinoid binding protein (Fragment).
GN IRBP.
OS Didelphis marsupialis virginiana (North American opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX NCBI_TaxID=9267;
RN [1]
RP SEQUENCE FROM N.A.
RA Jansa S.A., Voss R.S.;
RT "Phylogenetic studies on didelphid marsupials I. Introduction and
RT preliminary results from nuclear IRBP gene sequences.";
RL J. Mammal. Evol. 7:43-77(2000).
DR EMBL; AF257678; AAF72005.1; -.
DR InterPro; IPR003581; TSPC.
DR Pfam; PF02692; IRBP; 1.
DR SMART; SM00245; TSPC; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 386
SQ SEQUENCE 386 AA; 42197 MW; 121FCE422750DC91 CRC64;

Query Match 2.8%; Score 7; DB 6; Length 386;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 219 LHOGDIL 225
Db 141 LHOGDIL 147

RESULT 69

Q9NOS6 PRELIMINARY; PRT; 386 AA.
ID Q9NOS6
AC Q9NOS6;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE Interphotoreceptor retinoid binding protein (Fragment).
GN IRBP.
OS Chironectes minimus (water opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Chironectes.
OX NCBI_TaxID=91500;
RN [1]
RP SEQUENCE FROM N.A.
RA Jansa S.A., Voss R.S.;
RT "Phylogenetic studies on didelphid marsupials I. Introduction and
RT preliminary results from nuclear IRBP gene sequences.";
RL J. Mammal. Evol. 7:43-77(2000).
DR EMBL; AF257679; AAF72006.1; -.
DR InterPro; IPR003581; TSPC.
DR Pfam; PF02692; IRBP; 1.
DR SMART; SM00245; TSPC; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 386
SQ SEQUENCE 386 AA; 42169 MW; 3D026D50038CF12A CRC64;

Query Match 2.8%; Score 7; DB 6; Length 386;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 219 LHOGDIL 225
Db 141 LHOGDIL 147

RESULT 70

Q9NOS5 PRELIMINARY; PRT; 386 AA.
ID Q9NOS5
AC Q9NOS5;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE Interphotoreceptor retinoid binding protein (Fragment).
GN IRBP.
OS Marmosa lepida (little rufous mouse opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Marmosa.
OX NCBI_TaxID=126294;
RN [1]
RP SEQUENCE FROM N.A.
RA Jansa S.A., Voss R.S.;
RT "Phylogenetic studies on didelphid marsupials I. Introduction and
RT preliminary results from nuclear IRBP gene sequences.";
RL J. Mammal. Evol. 7:43-77(2000).
DR EMBL; AF257681; AAF72008.1; -.
DR InterPro; IPR003581; TSPC.
DR Pfam; PF02692; IRBP; 1.
DR SMART; SM00245; TSPC; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 386
SQ SEQUENCE 386 AA; 42118 MW; A5628DBF1626240B CRC64;

Query Match 2.8%; Score 7; DB 6; Length 386;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 219 LHOGDIL 225
Db 141 LHOGDIL 147

RESULT 71

Q9NOS4 PRELIMINARY; PRT; 386 AA.
ID Q9NOS4
AC Q9NOS4;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE Interphotoreceptor retinoid binding protein (Fragment).
GN IRBP.
OS Didelphis albiventris (white-eared opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX NCBI_TaxID=42716;
RN [1]
RP SEQUENCE FROM N.A.
RA Jansa S.A., Voss R.S.;
RT "Phylogenetic studies on didelphid marsupials I. Introduction and
RT preliminary results from nuclear IRBP gene sequences.";
RL J. Mammal. Evol. 7:43-77(2000).
DR EMBL; AF257682; AAF72009.1; -.
DR InterPro; IPR003581; TSPC.
DR Pfam; PF02692; IRBP; 1.
DR SMART; SM00245; TSPC; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 386
SQ SEQUENCE 386 AA; 42169 MW; 3D026D50038CF12A CRC64;

SQ SEQUENCE 386 AA; 42221 MW; 4B5F5B629CA2B62D CRC64;

Query Match

Best Local Similarity 2.8%; Score 7; DB 6; Length 386;
Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 219 LHQGDIL 225

Db 141 LHQGDIL 147

RESULT 72

O9NOS3

ID O9NOS3 PRELIMINARY; PRT; 386 AA.

AC O9NOS3; 01-OCT-2000 (TReMBLrel. 15, Created)

DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)

DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)

DE Interphotoreceptor retinoid binding protein (Fragment).

GN IRBP.

OS Didelphis albiventris (white-eared opossum).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.

OX NCBI_TaxID=42716;

RN [1]

RP SEQUENCE FROM N.A.

RA Jansa S.A., Voss R.S.;

RT "Phylogenetic studies on didelphid marsupials I. Introduction and

RT preliminary results from nuclear IRBP gene sequences.";

RL J. Mammal. Evol. 7:43-77(2000).

DR EMBL; AF257683; AAF72010.1; -.

DR InterPro; IPR003581; TSPC.

DR Pfam; PF02692; IRBP; 1.

DR SMART; SM00245; TSPC; 1.

KW Receptor.

FT NON_TER 1

FT NON_TER 386

SQ SEQUENCE 386 AA; 42277 MW; 2D624E6E331CC906 CRC64;

Query Match

Best Local Similarity 2.8%; Score 7; DB 6; Length 386;
Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 219 LHQGDIL 225

Db 141 LHQGDIL 147

SULT 73

NOS2

ID O9NOS2 PRELIMINARY; PRT; 386 AA.

AC O9NOS2; 01-OCT-2000 (TReMBLrel. 15, Created)

DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)

DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)

DE Interphotoreceptor retinoid binding protein (Fragment).

GN IRBP.

OS Lutreolina crassicaudata (thick-tailed opossum).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Lutreolina.

OX NCBI_TaxID=38620;

RN [1]

RP SEQUENCE FROM N.A.

RA Jansa S.A., Voss R.S.;

RT "Phylogenetic studies on didelphid marsupials I. Introduction and

RT preliminary results from nuclear IRBP gene sequences.";

RL J. Mammal. Evol. 7:43-77(2000).

DR EMBL; AF257684; AAF72011.1; -.

DR InterPro; IPR003581; TSPC.

DR Pfam; PF02692; IRBP; 1.

DR SMART; SM00245; TSPC; 1.

KW Receptor.

FT NON_TER 1

FT NON_TER 386

FT NON_TER 386 386
SQ SEQUENCE 386 AA; 42170 MW; 0C839B3F830C8AFD CRC64;

Query Match

Best Local Similarity 2.8%; Score 7; DB 6; Length 386;
Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 219 LHQGDIL 225

Db 141 LHQGDIL 147

RESULT 74

O9NOR8

ID O9NOR8 PRELIMINARY; PRT; 386 AA.

AC O9NOR8; 01-OCT-2000 (TReMBLrel. 15, Created)

DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)

DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)

DE Interphotoreceptor retinoid binding protein (Fragment).

GN IRBP.

OS Glironia venusta (bushy-tailed opossum).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Glironia.

OX NCBI_TaxID=42715;

RN [1]

RP SEQUENCE FROM N.A.

RA Jansa S.A., Voss R.S.;

RT "Phylogenetic studies on didelphid marsupials I. Introduction and

RT preliminary results from nuclear IRBP gene sequences.";

RL J. Mammal. Evol. 7:43-77(2000).

DR EMBL; AF257688; AAF72015.1; -.

DR InterPro; IPR003581; TSPC.

DR Pfam; PF02692; IRBP; 1.

DR SMART; SM00245; TSPC; 1.

KW Receptor.

FT NON_TER 1

FT NON_TER 386

SQ SEQUENCE 386 AA; 42040 MW; 9A0919B68FE48926 CRC64;

Query Match

Best Local Similarity 2.8%; Score 7; DB 6; Length 386;
Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 219 LHQGDIL 225

Db 141 LHQGDIL 147

RESULT 75

O9NOR6

ID O9NOR6 PRELIMINARY; PRT; 386 AA.

AC O9NOR6; 01-OCT-2000 (TReMBLrel. 15, Created)

DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)

DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)

DE Interphotoreceptor retinoid binding protein (Fragment).

GN IRBP.

OS Caluromys lanatus (western woolly opossum).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Caluromys.

OX NCBI_TaxID=42713;

RN [1]

RP SEQUENCE FROM N.A.

RA Jansa S.A., Voss R.S.;

RT "Phylogenetic studies on didelphid marsupials I. Introduction and

RT preliminary results from nuclear IRBP gene sequences.";

RL J. Mammal. Evol. 7:43-77(2000).

DR EMBL; AF257690; AAF72017.1; -.

DR InterPro; IPR003581; TSPC.

DR Pfam; PF02692; IRBP; 1.

DR SMART; SM00245; TSPC; 1.

KW Receptor.

4

FT NON_TER 1 1
FT NON_TER 386 386
SQ SEQUENCE 386 AA; 42178 MW; C6B9CF814D386624 CRC64;

Query Match 2.8%; Score 7; DB 6; Length 386;
Best Local Similarity 100.0%; Pred.No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 219 LHQGDIL 225
|||
Db 141 LHQGDIL 147

Search completed: March 26, 2003, 07:48:42
Job time : 96 secs

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 07:31:11 ; Search time 15 Seconds
(without alignments)
490.382 Million cell updates/sec

Title: US-09-724-341-8
Perfect score: 1304
Sequence: 1 MPASSPFLAPKGPFGNMG.....RARKLNLSPHGTFGLGVKL 250

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues
Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1304	100.0	250	US-08-883-086-2	Sequence 2, Appli
2	1296	99.4	250	US-09-153-927-4	Sequence 4, Appli
3	1285	98.5	247	US-09-157-864-4	Sequence 4, Appli
4	1195	91.6	234	US-09-157-864-2	Sequence 2, Appli
5	1031	79.1	205	US-09-286-529-5	Sequence 5, Appli
6	762	58.4	147	US-08-883-086-3	Sequence 3, Appli
7	710	54.4	136	US-09-589-287B-20	Sequence 20, Appli
8	244.5	18.8	285	US-09-589-287B-2	Sequence 1, Appli
9	244.5	18.8	266	US-09-589-287B-19	Sequence 19, Appli
10	231.5	17.8	219	US-09-589-287B-28	Sequence 28, Appli
11	227.5	17.4	219	US-09-589-287B-30	Sequence 30, Appli
12	210.5	16.1	289	US-09-589-287B-38	Sequence 38, Appli
13	210.5	16.1	145	US-09-286-529-21	Sequence 21, Appli
14	208	16.0	155	US-09-589-287B-23	Sequence 23, Appli
15	131	10.0	391	US-09-342-681C-2	Sequence 2, Appli
16	122	9.4	24	US-09-157-864-6	Sequence 80, Appli
17	112.5	8.6	155	US-07-994-469A-80	Sequence 4, Appli
18	110	8.4	377	US-09-342-681C-4	Sequence 77, Appli
19	108.5	8.3	155	US-07-994-469A-79	Sequence 79, Appli
20	107.5	8.2	155	US-07-994-469A-45	Sequence 45, Appli
21	107.5	8.2	155	US-07-994-469A-67	Sequence 67, Appli
22	107.5	8.2	155	US-07-994-469A-76	Sequence 76, Appli
23	107.5	8.2	155	US-07-994-469A-78	Sequence 78, Appli
24	107.5	8.2	154	US-07-994-469A-75	Sequence 86, Appli
25	107.5	8.2	154	US-07-994-469A-86	Sequence 86, Appli
26	106.5	8.2	158	US-07-994-469A-61	Sequence 61, Appli
27	106.5	8.2	163	US-07-994-469A-64	Sequence 13, Appli

28	106.5	8.2	158	6	5182196-2	Patent No. 5182196
29	106.5	8.2	161	1	US-07-994-469A-61	Sequence 61, Appli
30	106.5	8.2	163	1	US-07-994-469A-64	Sequence 64, Appli
31	105.5	8.1	150	1	US-07-668-517-13	Sequence 13, Appli
32	105.5	8.1	151	1	US-07-668-517-27	Sequence 27, Appli
33	105.5	8.1	158	1	US-07-994-469A-52	Sequence 52, Appli
34	105.5	8.1	176	6	5180811-12	Patent No. 5180811
35	103.5	7.9	145	1	US-07-994-469A-9	Sequence 9, Appli
36	103.5	7.9	155	1	US-07-994-469A-50	Sequence 50, Appli
37	103.5	7.9	155	1	US-07-994-469A-68	Sequence 68, Appli
38	103.5	7.9	157	1	US-07-668-517-33	Sequence 33, Appli
39	103.5	7.9	157	1	US-07-794-400-1	Sequence 1, Appli
40	103.5	7.9	157	1	US-08-041-648-2	Sequence 2, Appli
41	103.5	7.9	157	1	US-07-940-605A-5	Sequence 5, Appli
42	103.5	7.9	157	1	US-08-107-235-1	Sequence 1, Appli
43	103.5	7.9	157	1	US-08-217-529-2	Sequence 2, Appli
44	103.5	7.9	157	1	US-08-318-193-86	Sequence 86, Appli
45	103.5	7.9	157	1	US-08-397-470-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-08-883-086-2

Sequence 2, Application US/08883086

Patent No. 6171787

GENERAL INFORMATION:

APPLICANT: WILEY, STEVEN

TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL

TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Abbott Laboratories

STREET: 100 Abbott Park Road

CITY: Abbott Park

STATE: IL

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/883,086

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Porembski, Priscilla E.

REGISTRATION NUMBER: 33,207

REFERENCE/DOCKET NUMBER: 6134.US.01

TELECOMMUNICATION INFORMATION:

TELEPHONE: 847-937-0378

TELEFAX: 847-938-2623

TELEX:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 250 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: No. 6171787e

US-08-883-086-2

Query Match 100.0%; Score 1304; DB 4; Length 250;

Best Local Similarity 100.0%; Pred. No. 7.4e-133;

Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MPASSPFLAPKGPFGNMGVPREPALSVALWLSGALGAVACAMALLTQOTELQSLRR 60

DB 1 MPASSPFLAPKPGPGNMGVPVREPALSVALWLSWGALGAVACAMALLTQOTELQSLRR 60
QY 61 EVSRLQGTGPGSQNGEGYFWQSLPEQSSDALAEWENGERSRKRRAVLTQOKKQHSVLHL 120
DB 61 EVSRLQGTGPGSQNGEGYFWQSLPEQSSDALAEWENGERSRKRRAVLTQOKKQHSVLHL 120
QY 121 VPINATSKDDSDVTEVMQPALRRGRGLQAGGYVRIQDAGVYLLYSQVLFQDVTFTMGQ 180
DB 121 VPINATSKDDSDVTEVMQPALRRGRGLQAGGYVRIQDAGVYLLYSQVLFQDVTFTMGQ 180
QY 181 VVSREGQGRQETLFRICIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIPRARAKLNLSP 240
DB 181 VVSREGQGRQETLFRICIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIPRARAKLNLSP 240
QY 241 HGTFLGFVKL 250
DB 241 HGTFLGFVKL 250

Ne maveric laved

ULT 2
US-09-153-927-4
; Sequence 4, Application US/09153927A
; Patent No. 6297022
; GENERAL INFORMATION:
; APPLICANT: McDonnell, Peter C.
; APPLICANT: Young, Peter R.
; APPLICANT: Zou, Jun
; TITLE OF INVENTION: A Method of Identifying Agonists and
; TITLE OF INVENTION: Antagonists for Tumor Necrosis Related Receptors TR1, TR3
; TITLE OF INVENTION: and TR5
; FILE REFERENCE: GH50031
; CURRENT APPLICATION NUMBER: US/09/153,927A
; CURRENT FILING DATE: 1998-09-16
; EARLIER APPLICATION NUMBER: 60/061,334
; EARLIER FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Faeseq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Human
US-09-153-927-4

Query Match 99.4%; Score 1296; DB 4; Length 250;
Best Local Similarity 99.6%; Pred. No. 5.4e-132;
Matches 249; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DB 1 MPASSPFLAPKPGPGNMGVPVREPALSVALWLSWGALGAVACAMALLTQOTELQSLRR 60
QY 61 EVSRLQGTGPGSQNGEGYFWQSLPEQSSDALAEWENGERSRKRRAVLTQOKKQHSVLHL 120
DB 61 EVSRLQGTGPGSQNGEGYFWQSLPEQSSDALAEWENGERSRKRRAVLTQOKKQHSVLHL 120
QY 121 VPINATSKDDSDVTEVMQPALRRGRGLQAGGYVRIQDAGVYLLYSQVLFQDVTFTMGQ 180
DB 121 VPINATSKDDSDVTEVMQPALRRGRGLQAGGYVRIQDAGVYLLYSQVLFQDVTFTMGQ 180
QY 181 VVSREGQGRQETLFRICIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIPRARAKLNLSP 240
DB 181 VVSREGQGRQETLFRICIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIPRARAKLNLSP 240
QY 241 HGTFLGFVKL 250
DB 241 HGTFLGFVKL 250

RESULT 3
US-09-157-864-4
; Sequence 4, Application US/09157864
; Patent No. 6440694

GENERAL INFORMATION:
; APPLICANT: Bienkowski, Michael J
; APPLICANT: Mills, Cynthia J
; APPLICANT: Jones, David A
; TITLE OF INVENTION: TNF-Related Death Ligand
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pharmacia & Upjohn, Intellectual Property
; ADDRESSEE: Legal Services
; STREET: 301 Henrietta Street
; CITY: Kalamazoo
; STATE: MI
; COUNTRY: USA
; ZIP: 49001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/157,864
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerber, Lori L.
; REGISTRATION NUMBER: 41,113
; REFERENCE/DOCKET NUMBER: 6111.N CN1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 616/833-0974
; TELEFAX: 616/833-8897
; TELEX: 224401
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-157-864-4

Query Match 98.5%; Score 1285; DB 4; Length 247;
Best Local Similarity 100.0%; Pred. No. 8.2e-131;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 MPASSPFLAPKPGPGNMGVPVREPALSVALWLSWGALGAVACAMALLTQOTELQSLRR 60
QY 61 EVSRLQGTGPGSQNGEGYFWQSLPEQSSDALAEWENGERSRKRRAVLTQOKKQHSVLHL 120
DB 61 EVSRLQGTGPGSQNGEGYFWQSLPEQSSDALAEWENGERSRKRRAVLTQOKKQHSVLHL 120
QY 121 VPINATSKDDSDVTEVMQPALRRGRGLQAGGYVRIQDAGVYLLYSQVLFQDVTFTMGQ 180
DB 121 VPINATSKDDSDVTEVMQPALRRGRGLQAGGYVRIQDAGVYLLYSQVLFQDVTFTMGQ 180
QY 181 VVSREGQGRQETLFRICIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIPRARAKLNLSP 240
DB 181 VVSREGQGRQETLFRICIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIPRARAKLNLSP 240
QY 241 HGTFLG 246
DB 241 HGTFLG 246

RESULT 4
US-09-157-864-2
; Sequence 2, Application US/09157864
; Patent No. 6440694
; GENERAL INFORMATION:
; APPLICANT: Bienkowski, Michael J
; APPLICANT: Mills, Cynthia J
; APPLICANT: Jones, David A

```
/ TITLE OF INVENTION: TNF-Related Death Ligand
/ NUMBER OF SEQUENCES: 18
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pharmacia & Upjohn, Intellectual Property
/ ADDRESS: Legal Services
/ STREET: 301 Henrietta Street
/ CITY: Kalamazoo
/ STATE: MI
/ COUNTRY: USA
/ ZIP: 49001
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 Diskette
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ FILING DATE:
/ APPLICATION NUMBER: US/09/157,864
/ FILING DATE:
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Kerber, Lori L.
/ REGISTRATION NUMBER: 41,113
/ REFERENCE/DOCKET NUMBER: 6111.N CN1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 616/833-0974
/ TELEFAX: 616/833-8897
/ TELEX: 224401
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 234 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-09-157-864-2

Query Match          91.6%; Score 1195; DB 4; Length 234;
Best Local Similarity 92.8%; Pred. No. 4e-121;
Matches 232; Conservative 2; Mismatches 0; Indels 16; Gaps 1;

QY 1 MPASSPFLAPKGPNGNGPVRREPALSVALTWSGALGAVACAMALLTQOTELQSLR 60
DB 1 MPASSPFLAPKGPNGNGPVRREPALSVALTWSGALGAVACAMALLTQOTELQSLR 60
QY 61 EVSRLOGTGSPSONGEGYPWQSLPEQSSDALAEWENGERSRKRAVLTQKKOHVHL 120
DB 61 EVSRLOGTGSPSONGEGYPWQSLPEQSSDALAEWENGERSRKRAVLTQKKOHVHL 120
QY 121 VPINATSKDDSDVTEVMQPALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQ 180
DB 112 -----KNDSDVTEVMQPALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQ 164
QY 181 VVSREGQROETLFRCTIRSMPSHPDRAYNSCYSAGVFHLHOGDILSVIIPRARKNLSP 240
DB 165 VVSREGQROETLFRCTIRSMPSHPDRAYNSCYSAGVFHLHOGDILSVIIPRARKNLSP 224
QY 241 HGTFLGFVKL 250
DB 225 HGTFLGFVKL 234

RESULT 5
US-09-286-529-5
/ Sequence 5, Application US/09286529
/ Patent No. 6297367
/ GENERAL INFORMATION:
/ APPLICANT: Catherine Tribouley
/ TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
/ FILE REFERENCE: 1408.003/200130.439C1
/ CURRENT APPLICATION NUMBER: US/09/286,529
/ FILING DATE: 1999-04-05
/ NUMBER OF SEQ ID NOS: 25
/ SOFTWARE: FastSeq for Windows Version 3.0
```

```
/ SEQ ID NO 5
/ LENGTH: 205
/ TYPE: PRT
/ ORGANISM: human
/ US-09-286-529-5

Query Match          79.1%; Score 1031; DB 4; Length 205;
Best Local Similarity 98.0%; Pred. No. 1.7e-103;
Matches 201; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 46 MALLTQOTELQSLREVSRLOGTGSPSONGEGYPWQSLPEQSSDALAEWENGERSRKRA 105
DB 1 MVQLTQOTELQSLREVSRLOGTGSPSONGEGYPWQSLPEQSSDALAEWENGERSRKRA 60
QY 106 VLTQKKOHVHLVPINATSKDDSDVTEVMQPALRRGRGLQAQGYGVRIQDAGVYLL 165
DB 61 VLTQKKOHVHLVPINATSKDDSDVTEVMQPALRRGRGLQAQGYGVRIQDAGVYLL 120
QY 166 YSQLFQDVTFTMGQVSRREGQROETLFRCTIRSMPSHPDRAYNSCYSAGVFHLHOGDIL 225
DB 121 YSQLFQDVTFTMGQVSRREGQROETLFRCTIRSMPSHPDRAYNSCYSAGVFHLHOGDIL 180
QY 226 SVIIPRARKNLSPHGTFLGFVKL 250
DB 181 SVIIPRARKNLSPHGTFLGFVKL 205
```

```
RESULT 6
US-08-883-086-3
/ Sequence 3, Application US/08883086
/ Patent No. 6171787
/ GENERAL INFORMATION:
/ APPLICANT: WILEY, STEVEN
/ TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
/ NUMBER OF SEQUENCES: 13
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Abbott Laboratories
/ STREET: 100 Abbott Park Road
/ CITY: Abbott Park
/ STATE: IL
/ COUNTRY: USA
/ ZIP: 60064-3500
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/883,086
/ FILING DATE:
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Potembski, Priscilla E.
/ REGISTRATION NUMBER: 33,207
/ REFERENCE/DOCKET NUMBER: 6134.US.01
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 847-937-0378
/ TELEFAX: 847-938-2623
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 147 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: No. 6171787e
/ US-08-883-086-3

Query Match          58.4%; Score 762; DB 4; Length 147;
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! TYPE: PRT
; ORGANISM: Homo sapiens
US-09-589-287B-19

Query Match	17.8%	Score 232;	DB 4;	Length 266;
Best Local Similarity	28.5%	Pred. No. 5.6e-17;		
Matches 67;	Conservative 44;	Mismatches 78;	Indels 46;	Gaps 8;

[illegible]

```
QY    91 LEAME-----NGERSKRRAVLTKOKKHSHLHVPINATSKDSDVTEMMOPAL 142
      |::|         :|||          ::|   |||   :
Db    112 LKIEPPAPGEGNSSQRNRKRAV-----QGPEEFGSYTFVPWLSLF 153
```

```

QY 143 RRGKGLQAQGYGVRIODAGVLLYSQVLFDVTFTMGQVSR-----GQGRQETLFR 196
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 154 KRGSALAEKENKILVKEGYFFIYGQVLYTDKTYAMGHLQRKKVHVFGEDELSTVTLFR 213

```

```

197 IRSM- SHPDRAYNSCYSAGVHLLHQGDLSVII PRARAKNLSPHGTFLGFYKL 250
    ::::: : |||||: | :||: ||| :::: || :||
214 IONMPETLPN--NSCYSAGIAKLEEGDEIQLAIPRENAQISLDGDVTFPGALKL 265

```

RESULT 11
US-09-589-287B-28
Sequencia 28 Localização IIS/000000007B

```

; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Antibodies to Neutrokrine-alpha
; FILE REFERENCE: PF343P3C1
; CURRENT APPLICATION NUMBER: US/09/589,287B
; CURRENT FILING DATE: 2000-06-08
; Prior application data removed - check PALM or file wrapper
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 219
; TYPE: PRP
; ORGANISM: Homo sapiens
US-09-589-287B-28

```

Query Match	17.8%	Score 231.5;	DB 4;	Length 219;
Best Local Similarity	29.8%	Pred. No. 4.7e-17;		
Matches 70; Conservative	35;	Mismatches 71;	Indels 59;	Gaps 8;

```

52 QTELQSLRREVSRLOG-----TGG-----PSQNGEGYPMQSL 83
   | : | | | | | | | | | | | | | | | | | | | |
7  QGSLASLRAE---LQGHHAELKLPARARAPKAGLGEAPAVTAGLKIFEPAPGEGNSSQS - 62

```

[illegible]

```

QY 143 RRGRLQAQGYGVRIQDAVLLYSQVLFDVTFMGVVSRE-----GQGRQETLRC 196
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 107 KRGSALEEKENKILVKTGYFFIYGQVLYTDKTYAMGHLQRKKVHVFGEDELSVTLERC 166

```

```
QY 197 IRSM- SHPDRAYNSCYSAGVFLHQGDILVII PRARAKNLUSPHGTFLGFYKL 250
    :::: : |::::: | :||| : ||| :|::
Db 167 IONMPETLPN-- NSCYSAGIAKLEEGDELQLAIPRENAQISLDGDTVTFGALUKL 218
```

RESULT 12
US-09-589-287B-30
: Sequence 30. Application IIS/095A9287B

```

;
;   APPLICANT: Yu et al.
;   TITLE OF INVENTION: Antibodies to Neutrokin-alpha
;   FILE REFERENCE: PF343P3C1

```

```

; CURRENT APPLICATION NUMBER: US/09/589,287B
; CURRENT FILING DATE: 2000-06-08
; Prior application data removed - check PALM or file wrapper
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30

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; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-589-287B-30

Query Match	17.4%;	Score 227.5;	DB 4;	Length 219;
Best Local Similarity	28.7%;	Pred. No. 1.3e-16;		
Matches	64;	Conservative	46;	Mismatches 78;
				Indels 35;
				Gaps 7;

```

QY      52 QTELQSLRREVSRLOCTGSPSQNGEGIPWQSLPEQS-----SDALEAWE----- 95
      | : | | | | : | : | : | : | : |
Db      7 QGDPLASLRLEIQ-----SHHAEXUPARARAPAKGLGEAPAVTAGLKIFEEPPAPGEGN 58

```

QY 96 NGEHSRKRAVLTKQKQHSHLVLPINAT-SKDDSDVTEVMVPALRRGRGLQAQGYG 154
 ::|::|::|::|::|::|::|::|::|:
Db 59 SSGSSRNKRPAICGAEEVTIQDCIQLIADETPTTIQGSGSYTFVPMILSFKRGSALEEKENK 118

```

QY 155 VR1QDAGVYLLYSQVLFDVTFMGQVSR-----GGGRQETLFCRISRMP-SHPDRA 207
      : :: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 119 ILVETGYFFIYGQVLYTDKTYANGHLIQKKVHVFGEDELSLVTLFCRIQMPEILPN-- 176

```

QY 208 YNCSYSAGVFLHQCGLISVIIIPARAKLTNSPHGIFLGFKL 250
| | | | : | : | | : | : | | | : |
Db 177 -NCYSAGIAKEEGDELQLAIPRENAQISLDGDVTFFGALKL 218

RESULT 13
US-09-589-287B-38
: Sequence 38, Application US/09589287B

```

; TITLE OF INVENTION: Antibodies to Neutrokrine-alpha
; FILE REFERENCE: PF343P3C1
; CURRENT APPLICATION NUMBER: US/09/589,287B
; CURRENT FILING DATE: 2000-06-08
; Prior application data removed - check PALM or file wrapper
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-589-287B-38

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Query Match	16.1%;	Score 210.5;	DB 4;	Length 289;
Best Local Similarity	28.0%;	Pred. No. 1.3e-14;		
Matches	76;	Conservative	45;	Mismatches 109;
			Indels	41;
			Gaps	10;

QY 9 LAKPGPPGNMGSPVREPALSVALLMWLSGALGVACAMA---LLTQOTELQSRLREVSRRL 65
 :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Db 30 ITPQKEEGAMFGICRDRGLAATLLL--ALLSSEFTAMSLYLQALQADLMNRMELQSY 87

```

QY 66 QGTGSPSQNGEGTPWQSLPEQS-----SDALEMENGERS-RRRRAVLTKQKKQHSVL 118
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 88 RGSATPAAAG-----APELTAGVKLLTPAADRPNNSSRGHRNRRAFGQPEETEDVDVL 140

```

```

QY      119  HLPV-----INATSKDDSD-----VTEVMWQPALRRGRGLDAGSGVRIQDAGVLLY 166
Db      141  SAPAPCLPGCRHSQHDDNGMNLRNIIQDCLOLTADSDTPALEEKENKIIVRQIGYFFIY 200

```

```

QY 167 SQVLEQDVTFIMGQVSKR-----GQGRQELTFRCIKRMP--SHEDRAINSCTISAGVFHL 219
Db 201 SQVLYTDPIFAMGHVIGRKKAHVFGDELSLTFELRCIQNMKPLPN---NSCYSGIARL 257

```

QY 220 HOGDLSVIIPRAKLNLSPHGTFGLGVKL 250
 :|| : : ||| |::: : ||| :||

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 07:34:09 ; Search time 36 Seconds
(without alignments)
925.352 Million cell updates/sec

Title: US-09-724-341-8
Perfect score: 250
Sequence: 1 MPASSPFLAPKGPFGMG.....RARKLNLSPHGTFLEVKL 250

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues
rd size : 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database : A_Geneseq_101002:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	250	100.0	250	20	AAV06485 Human tumour-asso
2	250	100.0	250	20	AAV17832 Human PRO715 prote
3	250	100.0	250	20	AAV04283 Human APRIL protei
4	250	100.0	250	20	AAW88368 Tumour necrosis fa
5	250	100.0	250	21	AAV93692 Amino acid sequenc
6	250	100.0	250	21	AAAB01323 Human PRO715 polyp
7	250	100.0	250	22	AAE09243 Human APRIL protei
8	250	100.0	250	22	AAAB62329 Human TRDL-1alpha
9	250	100.0	250	22	AAV71981 Human TNF and Apol
10	250	100.0	250	23	AAV99305 Human tumour necro

11	250	100.0	250	23	ABB81486 Human ZTNF2 amino
12	250	100.0	250	23	ABP47228 Human Blys binding
13	250	100.0	250	23	AAU79155 Human APRIL (a pro
14	246	98.4	247	20	AAV28836 Human TNF-related
15	246	98.4	247	22	AAB62327 Human TRDL-1gamma
16	202	80.8	205	20	AAV22225 Human tumour necro
17	183	73.2	233	23	AAU75402 Tumour necrosis fa
18	183	73.2	233	23	AAU75402 Tumour necrosis fa
19	183	73.2	250	20	AAV05745 Human tumour necro
20	183	73.2	250	23	AAU99510 Human tumour necro
21	154	61.6	233	20	AAV09551 Human TRAILK-3 pr
22	154	61.6	233	20	AAU75406 Human tumour necro
23	154	61.6	250	20	AAW93588 Human TNRL1-beta p
24	154	61.6	250	21	AAV79670 Human death recept
25	154	61.6	260	20	AAE15502 Human APRIL G70 pr
26	154	61.6	260	20	AAV60542 Human normal bladd
27	154	61.6	260	21	AAE15482 Human pancreatic c
28	152	60.8	248	23	AAE15482 Human APRIL G70 pr
29	147	58.8	147	20	AAW88369 Tumour necrosis fa
30	146	58.4	177	23	AAO14134 Protein of a FLAG
31	142	56.8	172	22	AAE00505 FLAG-human A Proli
32	142	56.8	233	18	AAW37002 Human tumour necro
33	136	54.4	136	21	AAW08661 Human APRIL (a pro
34	136	54.4	136	23	AAU79142 Human APRIL protei
35	130	52.0	248	22	AAE07877 Gene 44 human secr
36	123	49.2	123	22	AAE07877 Human tumour necro
37	121	48.4	168	18	AAW37003 Tumour necrosis fa
38	121	48.4	168	23	AAU99509 Tumour necrosis fa
39	121	48.4	168	23	AAU75403 Human TRDL-1beta p
40	121	48.4	234	20	AAV28835 Human tumour necro
41	121	48.4	234	22	AAV79672 Tumour necrosis fa
42	121	48.4	234	23	AAU99511 Human prostate tum
43	121	48.4	234	23	AAU75407 Mouse FLAG-tagged
44	121	48.4	244	20	AAV74026 Protein of a FLAG-
45	21	8.4	149	23	AAE15499 Human-mouse APRIL
46	21	8.4	199	23	AAE15503 Mouse APRIL protei
47	21	8.4	232	20	AAV04284 Mouse death recept
48	21	8.4	232	21	AAV79672 Mouse APRIL protei
49	21	8.4	232	22	AAE07878 Murine myc tagged
50	21	8.4	232	22	AAE07878 Mouse TNRL1-beta p
51	21	8.4	234	22	AAE00504 Mouse APRIL/G70 pr
52	21	8.4	240	23	AAE15483 Protein of a myc-t
53	21	8.4	241	20	AAW93589 Human TRDL-1gamma
54	21	8.4	249	23	AAO14131 Arabidopsis thalia
55	14	5.6	15	22	AAB62328 Insulin/insulin-li
56	8	3.2	184	21	AAV07407 Amino acid sequenc
57	8	3.2	223	21	AAB18748 Dermaseptin B amin
58	7	2.8	20	23	AAV90178 A mature dermas
59	7	2.8	20	23	AAU90722 Lipase signal pept
60	7	2.8	27	21	AAE18725 Human immune/haema
61	7	2.8	31	21	AAB18725 Eucalyptus grandis
62	7	2.8	31	21	AAB12436 Novel human diagno
63	7	2.8	32	21	AAB18748 Human immune/haema
64	7	2.8	45	19	AAW34538 A dermas
65	7	2.8	61	22	AAE0507
66	7	2.8	62	21	AAE16374
67	7	2.8	65	22	ABG12905
68	7	2.8	73	22	AAE04103
69	7	2.8	78	21	AAE18724
70	7	2.8	79	22	AAE64816
71	7	2.8	83	22	AAE89786
72	7	2.8	87	22	AAU44493
73	7	2.8	96	20	AAW82267
74	7	2.8	96	20	AAW82267
75	7	2.8	105	22	AAO08276
76	7	2.8	127	22	AAE64874
77	7	2.8	133	23	AAV79152
78	7	2.8	141	21	AAV71040
79	7	2.8	142	21	AAE08258
80	7	2.8	142	21	AAE58966
81	7	2.8	142	23	AAU10946
82	7	2.8	144	21	AAB08270
83	7	2.8	144	21	AAV97038

84	7	2.8	147	21	AAB08271	Amino acid sequenc
85	7	2.8	147	22	ABB12145	Human liver cell p
86	7	2.8	150	19	AAW62463	Mouse T cell surfa
87	7	2.8	152	23	AAU79149	Rat Neurokine- α p
88	7	2.8	153	21	AAV97036	Soluble human TNF
89	7	2.8	153	21	AAAG10136	Arabidopsis thalia
90	7	2.8	155	21	AAAB08714	A murine neutrokin
91	7	2.8	155	21	AAV71044	Streptococcus pyog
92	7	2.8	155	23	AAU79143	Mouse Neurokine-a
93	7	2.8	158	19	AAW81328	TNF2-3, a TNF-alph
94	7	2.8	158	22	ABB76582	Human TNFAD3. Homo
95	7	2.8	158	23	ABB02726	Human TNF-alpha an
96	7	2.8	159	21	AAV71041	Streptococcus pyog
97	7	2.8	163	21	AAAG21362	Zea mays protein f
98	7	2.8	165	23	AAU79150	Rat Neurokine- α p
99	7	2.8	167	21	AAV71046	Streptococcus pyog
100	7	2.8	177	21	AAB08664	A murine neutrokin

ALIGNMENTS

RESULT 1

AAV06485 ID AAY06485 standard; Protein; 250 AA.

AC AAY06485;

DT 27-SEP-1999 (first entry)

DE Human tumour-associated protein PRO715.

XX PRO715; UNQ383; cancer; tumour necrosis family; diagnosis; therapy;
KM human.

OS Homo sapiens.

XX WO9935170-A2.

PD 15-JUL-1999.

XX 05-JAN-1999; 99WO-US00106.

PR 20-NOV-1998; 98US-0109304.

PR 05-JAN-1998; 98US-0070440.

PR 29-APR-1998; 98US-0083500.

PR 22-MAY-1998; 98US-0086414.

PR 10-JUN-1998; 98US-0088742.

PR 10-NOV-1998; 98US-0107783.

DR N-PSDB; AAX87262.

XX Antibody against proteins expressed in neoplastic cells, useful for
PT tumour diagnosis and treatment

XX Example 1; Fig 18; 162pp; English.

CC This sequence represents human PRO715 (UNQ382), a protein encoded
CC by the novel cDNA clone DNA52722 (see AAX87262) that shows homology
CC to members of the tumour necrosis factor family. Amplification of
CC DNA52722 was observed in various colon and lung tumors and cell
CC lines, suggesting a role in tumour formation or growth. Antagonists
CC (e.g. antibodies) directed to PRO715 may have use in cancer therapy.
CC The invention identifies 14 genes (see AAX87254-67) that are amplified
CC in the genome of tumour cells. Such amplification is expected to be
CC associated with overexpression of the gene product and to contribute
CC to tumorigenesis. The encoded proteins (see AAY06477-90) may be

CC useful targets for the diagnosis and/or treatment (including
CC prevention) of certain cancers, and may act as predictors of the
CC prognosis of tumour treatment. Antibodies that bind the proteins
CC are claimed and used in claimed cancer diagnostic kits.

XX SQ Sequence 250 AA;

Query Match 100.0%; Score 250; DB 20; Length 250;
Best Local Similarity 100.0%; Pred. No. 2e-234;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPASSPFLLPKPGPGNMGGPVREPALSVALLWSGALGAVACAMALLTQOTELQSLR 60

DB 1 MPASSPFLLPKPGPGNMGGPVREPALSVALLWSGALGAVACAMALLTQOTELQSLR 60

QY 61 EVSRLOGTGPGSQNGEGYPWQSLPEQSSDALAEWNGERSRKRRAVLTKQKKQSVLHL 120

DB 61 EVSRLOGTGPGSQNGEGYPWQSLPEQSSDALAEWNGERSRKRRAVLTKQKKQSVLHL 120

QY 121 VPINATSKDSDVTEVMQPALRRGRLQAGYVRIQDAGVYLLYSQVLFQDVFTMGQ 180

DB 121 VPINATSKDSDVTEVMQPALRRGRLQAGYVRIQDAGVYLLYSQVLFQDVFTMGQ 180

QY 181 VVSREGQGRQETLPRCIRSMPSHPDRAVNSCYSGAVFHLHOGDLSVILPRARAKNLSP 240

DB 181 VVSREGQGRQETLPRCIRSMPSHPDRAVNSCYSGAVFHLHOGDLSVILPRARAKNLSP 240

QY 241 HGTFLGFVKL 250

DB 241 HGTFLGFVKL 250

RESULT 2

AAV17832 ID AAY17832 standard; Protein; 250 AA.

AC AAY17832;

DT 12-AUG-1999 (first entry)

DE Human PRO715 protein sequence.

XX Human; PRO protein; tumour necrosis factor family; TNF; cytokine;
KW secreted protein; transmembrane protein; inflammation disorder.

OS Homo sapiens.

XX WO9928462-A2.

PD 10-JUN-1999.

XX 01-DEC-1998; 98WO-US25108.

PR 25-FEB-1998; 98US-0075945.

PR 03-DEC-1997; 97US-0067411.

PR 11-DEC-1997; 97US-0069278.

PR 11-DEC-1997; 97US-0069334.

PR 11-DEC-1997; 97US-0069335.

PR 12-DEC-1997; 97US-0069425.

PR 16-DEC-1997; 97US-0069694.

PR 16-DEC-1997; 97US-0069696.

PR 17-DEC-1997; 97US-0069702.

PR 17-DEC-1997; 97US-0069870.

PR 18-DEC-1997; 97US-0068017.

PR 05-JAN-1998; 98US-0070440.

PR 09-FEB-1998; 98US-0074086.

PR 09-FEB-1998; 98US-0074092.

XX (GETH) GENENTECH INC.

XX Baker KP, Chen J, Goddard A, Gurney AL, Wood WI;
PI Yuan J;

XX WPI; 1999-371118/31.
DR N-PSDB; AAX80057.
XX
PT Nucleic acids encoding PRO secreted and transmembrane proteins
XX
PS Claim 12; Fig 31; 123pp; English.
XX
CC The present invention describes nucleic acids encoding PRO secreted and
CC transmembrane proteins used therapeutically. The PRO proteins have
CC cyostatic, anti-inflammatory, anti-proliferative and immunosuppressive
CC activity. The proteins and polynucleotides can be used in therapy,
CC identification of homologues, raising antibodies and design of probes
CC and primers. They can be used in a range of diseases related to proteins
CC that they have homology with, e.g. a PRO protein having homology to
CC complement proteins may be used in inflammatory responses.
XX
SQ Sequence 250 AA;

Query Match 100.0%; Score 250; DB 20; Length 250;
Best Local Similarity 100.0%; Pred. No. 2e-234;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MPASSPFLAPKPPGNGGVPREPALSVLWLSWGAALGAVACAMALLTQOTELQSLRR 60
DB 1 MPASSPFLAPKPPGNGGVPREPALSVLWLSWGAALGAVACAMALLTQOTELQSLRR 60
OY 61 EVSRLQGTGSPSQNGEGYPWQSLPEQSSDALAEWNGERSRKRRAVLTQKKQHSVLHL 120
DB 61 EVSRLQGTGSPSQNGEGYPWQSLPEQSSDALAEWNGERSRKRRAVLTQKKQHSVLHL 120
OY 121 VPINATSKDSDVTEVMWQPALRRGRLQAGYGVRIQDAGVYLLYSQVLFQDVTFTMGQ 180
DB 121 VPINATSKDSDVTEVMWQPALRRGRLQAGYGVRIQDAGVYLLYSQVLFQDVTFTMGQ 180
OY 181 VVSREGQGRQETLFRICIRSMPSHPDRAYNSCYAGVFHLHOGDILSVIIPRARA KLNLS P 240
DB 181 VVSREGQGRQETLFRICIRSMPSHPDRAYNSCYAGVFHLHOGDILSVIIPRARA KLNLS P 240
OY 241 HGTFLGFVKL 250
DB 241 HGTFLGFVKL 250

RESULT 3
AAY04283
ID AAY04283 standard; Protein; 250 AA.

AAY04283;

DT 17-JUN-1999 (first entry)
XX
DE Human APRIL protein sequence.
XX
KW APRIL; tumour necrosis factor; TNF; proliferating inducing agent;
KW immune disorder; cancer.
XX
OS Homo sapiens.
XX
PN WO912965-A2.
XX
PD 18-MAR-1999.
XX
PF 11-SEP-1998; 98WO-US19191.
XX
PR 26-MAR-1998; 98US-0079384.
PR 12-SEP-1997; 97US-0058786.
XX
PA (BIOJ) BIOGEN INC.
XX
PI Tschopp J;
XX
DR WPI; 1999-215028/18.

DR N-PSDB; AAX30124.
XX
PT A Proliferating Inducing Agent (APRIL), a member of the Tumour
PT Necrosis Factor Family - useful as diagnostic agents and for
PT prevention or treatment of immune disorders and cancer
XX
PS Claim 12; Page 46; 47pp; English.
XX

CC The present sequence represents a proliferating inducing agent (APRIL)
CC isolated from human. APRIL is a member of the tumour necrosis factor
CC family, and essentially free of normally associated proteins. APRIL and
CC APRIL antibodies are useful in pharmaceutical compositions for
CC preventing or reducing severity of an autoimmune disease or an immune
CC response to tissue graft. The composition is also useful for stimulating
CC or suppressing the immune system, and treating cancer. APRIL is also
CC useful for treating APRIL-related disorders by delivering via a vector
CC (preferably viral vector) (gene therapy) into a mammalian (preferably
CC human) cell. Labeled APRIL and fragments are useful for identifying
CC APRIL receptors by screening compositions. Antisense DNA and antibodies
CC and modified APRIL (preferably an anti-APRIL receptor antibody) are
CC useful as blocking agents for inducing cell death by interfering with
CC APRIL receptors. The blocking agent is preferably administered with
CC interferon- γ and treats, suppresses or alters an immune response
CC involving a signalling pathway between APRIL and its receptor
CC (preferably involving human carcinoma cells); and also treats,
CC suppresses or alters the progression of cancer (preferably at least one
CC chemotherapeutic agent is also administered, and radiation therapy is
CC also given to the patient.
XX
SQ Sequence 250 AA;

Query Match 100.0%; Score 250; DB 20; Length 250;
Best Local Similarity 100.0%; Pred. No. 2e-234;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MPASSPFLAPKPPGNGGVPREPALSVLWLSWGAALGAVACAMALLTQOTELQSLRR 60
DB 1 MPASSPFLAPKPPGNGGVPREPALSVLWLSWGAALGAVACAMALLTQOTELQSLRR 60
OY 61 EVSRLQGTGSPSQNGEGYPWQSLPEQSSDALAEWNGERSRKRRAVLTQKKQHSVLHL 120
DB 61 EVSRLQGTGSPSQNGEGYPWQSLPEQSSDALAEWNGERSRKRRAVLTQKKQHSVLHL 120
OY 121 VPINATSKDSDVTEVMWQPALRRGRLQAGYGVRIQDAGVYLLYSQVLFQDVTFTMGQ 180
DB 121 VPINATSKDSDVTEVMWQPALRRGRLQAGYGVRIQDAGVYLLYSQVLFQDVTFTMGQ 180
OY 181 VVSREGQGRQETLFRICIRSMPSHPDRAYNSCYAGVFHLHOGDILSVIIPRARA KLNLS P 240
DB 181 VVSREGQGRQETLFRICIRSMPSHPDRAYNSCYAGVFHLHOGDILSVIIPRARA KLNLS P 240
OY 241 HGTFLGFVKL 250
DB 241 HGTFLGFVKL 250

RESULT 4
AAW88368
ID AAW88368 standard; Protein; 250 AA.

AAW88368;

DT 26-APR-1999 (first entry)
XX
DE Tumour necrosis factor-gamma.
XX
KW Tumour necrosis factor-gamma; TNF-gamma; human; inflammation;
KW cancer; tumour; metastasis; graft versus host disease;
KW drug screening; therapy; diagnosis.
XX
OS Homo sapiens.
XX
PN WO9900518-A1.

XX 07-JAN-1999.
PD
XX
PF 12-JUN-1998; 98WO-US12101.
XX
PR 26-JUN-1997; 97US-0883086.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Wiley SR;
XX
DR WPI; 1999-095761/08.
DR N-PSDB; AAX06771.
XX
PT Tumour necrosis factor gamma detects target polynucleotides - useful
PT for, e.g. treating inflammation, cancer and graft versus host
PT disease
XX
PS Claim 16; Page 84-85; 106pp; English.

This is the amino acid sequence of human tumour necrosis factor gamma (TNFG), a novel member of the TNF family of ligands. The invention provides a method of producing TNFG polypeptide using a recombinant expressing system comprising a nucleic acid sequence (see AAX06771) encoding TNFG and transformed host cells. Also provided are a procedure of producing biologically active soluble TNFG (see AAW88369), which can be used to treat deficiencies of TNFG and disease conditions ameliorated by TNFG. Antibodies, antagonists and inhibitors of such a polypeptide may be used to treat TNFG-associated diseases, tumours or metastases, and to screen for, diagnose and monitor conditions attributable to TNFG, especially inflammation, cancer and graft versus host disease. Cells expressing TNFG on their surface can be used to screen for (ant)agonists, and to detect receptor binding.

XX Sequence 250 AA;

Query Match 100.0%; Score 250; DB 20; Length 250;
Best Local Similarity 100.0%; Pred. No. 2e-234;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPASSPFLAPKGPNGMGVREPALSVLWLSWGALGAVACAMALLTQOTELQSLRR 60
Db 1 MPASSPFLAPKGPNGMGVREPALSVLWLSWGALGAVACAMALLTQOTELQSLRR 60
QY 61 EVSRLQGTGSPSONGEGYPWQSLPEQSSDALAEWENGERSRKRRAVLTKQKQKSHVHL 120
Db 61 EVSRLQGTGSPSONGEGYPWQSLPEQSSDALAEWENGERSRKRRAVLTKQKQKSHVHL 120
QY 121 VPINATSKDSDVTEVMMQPALRRGRLAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQ 180
Db 121 VPINATSKDSDVTEVMMQPALRRGRLAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQ 180
QY 181 VVSREGQGRQETLFRICRSMPSHPDRAYNCSYAGVFHLLHOGDILSVITPRARAKNLSP 240
Db 181 VVSREGQGRQETLFRICRSMPSHPDRAYNCSYAGVFHLLHOGDILSVITPRARAKNLSP 240
QY 241 HGTFLGFVKL 250
Db 241 HGTFLGFVKL 250

RESULT 5
ID AAY93692 standard; Protein; 250 AA.
XX
AC AAY93692;
XX
DT 03-OCT-2000 (first entry)
XX
DE 'Amino acid sequence of novel polypeptide PRO715.
XX
KW PRO201; PRO292; PRO327; PRO1265; PRO344; PRO343; PRO347; PRO357;

KW PRO715; PRO1017; PRO1112; PRO509; PRO853; PRO882; tumour cell;
KW tumorigenesis; cancer; neoplastic cell growth; cell proliferation.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..40
FT /note= "signal sequence"
FT 34..45
FT Region /note= "prokaryotic membrane lipoprotein attachment site"
FT 36..42
FT Modified-site /note= "N-myristoylation site"
FT Modified-site 40..46
FT Modified-site /note= "N-myristoylation site"
FT Modified-site 124..128
FT Modified-site /note= "N-glycosylation site"
FT Modified-site 156..164
FT Modified-site /note= "tyrosine kinase phosphorylation site"
FT Modified-site 179..185
FT /note= "N-myristoylation site"
FT Modified-site 242..248
FT /note= "N-myristoylation site"

XX WO200037640-A2.
XX
XX 29-JUN-2000.
XX
XX 16-DEC-1999; 99WO-US30095.
XX
XX 22-DEC-1998; 98US-0113296.
XX 08-MAR-1999; 99WO-US05028.
XX 02-JUN-1999; 99WO-US12252.
XX 01-SEP-1999; 99WO-US20111.
XX 15-SEP-1999; 99WO-US21090.
XX 30-NOV-1999; 99WO-US28313.
XX 30-NOV-1999; 99WO-US28409.
XX 01-DEC-1999; 99WO-US28301.
XX 02-DEC-1999; 99WO-US28565.
XX
XX (GETH) GENENTECH INC.
XX
XX Botstein D, Goddard A, Gurney AL, Hillan K, Lawrence DA, Roy MA;
XX Wood WI;
XX
XX WPI; 2000-452188/39.
XX
XX N-PSDB; AAA46928.
XX

PT New anti-polypeptide antibody useful in the treatment and diagnosis of
PT neoplastic cell growth and proliferation -
XX

PS Claim 61; Fig 18; 220pp; English.

XX The present sequence represents a novel human polypeptide. The
XX specification describes novel polypeptides designated PRO201, PRO292,
XX PRO327, PRO1265, PRO344, PRO343, PRO347, PRO357, PRO1017,
XX PRO1112, PRO509, PRO853 and PRO882. These genes are amplified in
XX the genome of tumour cells. The polypeptides are believed to contribute
XX to tumorigenesis. The polypeptides are useful target for the
XX identification of certain cancers, and may act as predictors of the
XX prognosis of tumour treatment. Antibodies against these polypeptides
XX are useful in the treatment and diagnosis of neoplastic cell growth
XX and proliferation in mammals.

XX Sequence 250 AA;

Query Match 100.0%; Score 250; DB 21; Length 250;
Best Local Similarity 100.0%; Pred. No. 2e-234;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPASSPFLAPKGPNGMGVREPALSVLWLSWGALGAVACAMALLTQOTELQSLRR 60
Db 1 MPASSPFLAPKGPNGMGVREPALSVLWLSWGALGAVACAMALLTQOTELQSLRR 60

Qy 61 EVSRLQGTGSPSQNGEGYPWQSLPEQSSDALEAWENGERSRKRRAVLTKQKKQHSVLHL 120
Db 61 EVSRLQGTGSPSQNGEGYPWQSLPEQSSDALEAWENGERSRKRRAVLTKQKKQHSVLHL 120
Qy 121 VPINATSKDSDVTEVMQPALRRGRLQAGYGVRIQDAGVYLLYSQVLFQDVFTMGQ 180
Db 121 VPINATSKDSDVTEVMQPALRRGRLQAGYGVRIQDAGVYLLYSQVLFQDVFTMGQ 180
Qy 181 VVSREGQGRQETLFRICRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIPRARA KNLSP 240
Db 181 VVSREGQGRQETLFRICRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIPRARA KNLSP 240
Qy 241 HGTFLGFVKL 250
Db 241 HGTFLGFVKL 250
RESULT 6
AAB01323 standard; Protein; 250 AA.
AAB01323;
XX 25-SEP-2000 (first entry)
DE Human PRO715 polypeptide.
XX
KW PRO; membrane bound protein; secreted protein; PRO357; PRO327;
KW PRO243; PRO715; PRO241; PRO323; PRO299; PRO233; PRO344; PRO347;
KW PRO355; PRO353; PRO361; PRO365; transmembrane polypeptide;
KW antibody; screening; detection; inhibition; probe; primer; human.
XX
OS Homo sapiens.
XX
FH Key location/Qualifiers
FT Peptide 1..40
FT Domain /label= Signal peptide
FT 34..45
FT /label= Prokaryotic membrane lipoprotein lipid
FT attachment site
FT Modified-site 36..42
FT /note= "N-myristoylation site"
FT Modified-site 40..46
FT /note= "N-myristoylation site"
FT Modified-site 124..128
FT /note= "N-glycosylation site"
FT Modified-site 156..164
FT /note= "Tyrosine kinase phosphorylation site"
FT Modified-site 179..185
FT /note= "N-myristoylation site"
FT Modified-site 242..248
FT /note= "N-myristoylation site"
FT
XX WO200032776-A2.
XX
XX 08-JUN-2000.
XX
XX PF 01-DEC-1999; 99WO-US28301.
XX
XX PR 01-DEC-1998; 98WO-US25108.
XX PR 16-DEC-1998; 98US-0112850.
XX PR 22-DEC-1998; 98US-0113296.
XX
XX PA (GETH) GENENTECH INC.
XX
PI Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;
PI Geritsen ME, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;
PI Hillan KJ, Kijavirij, Napier MA, Roy MA, Tumas D, Wood WI;
XX
XX WPI; 2000-412324/35.
XX DR N-PSDB; AAA49565.
XX
PT New human nucleic acids encoding secreted and transmembrane

PT polypeptides, designated as PRO polypeptides, useful as pharmaceutical
PT and diagnostic agents
XX
PS Claim 12; Fig 28; 187pp; English.
XX
CC New human nucleic acids encoding secreted and transmembrane
CC polypeptides which are designated as PRO polypeptides are described
CC The membrane-bound proteins have various industrial applications,
CC including as pharmaceutical and diagnostic agents. The membrane-bound
CC proteins can also be employed for screening of potential peptide or
CC small molecule inhibitors of the relevant receptor/ligand interaction.
CC Anti-PRO antibodies are useful for the affinity purification of PRO
CC from recombinant cell culture or natural sources.
XX
SQ Sequence 250 AA;
Query Match 100.0%; Score 250; DB 21; Length 250;
Best Local Similarity 100.0%; Pred. No. 2e-234;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPASSPFLAPKPGPNMGVPREPALSVALWLSWGALGAVACAMALLTQOTELQSLRR 60
Db 1 MPASSPFLAPKPGPNMGVPREPALSVALWLSWGALGAVACAMALLTQOTELQSLRR 60
Qy 61 EVSRLQGTGSPSQNGEGYPWQSLPEQSSDALEAWENGERSRKRRAVLTKQKKQHSVLHL 120
Db 61 EVSRLQGTGSPSQNGEGYPWQSLPEQSSDALEAWENGERSRKRRAVLTKQKKQHSVLHL 120
Qy 121 VPINATSKDSDVTEVMQPALRRGRLQAGYGVRIQDAGVYLLYSQVLFQDVFTMGQ 180
Db 121 VPINATSKDSDVTEVMQPALRRGRLQAGYGVRIQDAGVYLLYSQVLFQDVFTMGQ 180
Qy 181 VVSREGQGRQETLFRICRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIPRARA KNLSP 240
Db 181 VVSREGQGRQETLFRICRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIPRARA KNLSP 240
Qy 241 HGTFLGFVKL 250
Db 241 HGTFLGFVKL 250
RESULT 7
AAE09243
ID AAE09243 standard; Protein; 250 AA.
XX
XX AC AAE09243;
XX
XX DT 19-NOV-2001 (first entry)
XX
DE Human APRIL protein.
XX
KW Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor;
KW TNFR; TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis;
KW psoriasis.
XX
XX OS Homo sapiens.
XX
XX PN WO200160397-A1.
XX
XX PD 23-AUG-2001.
XX
XX PF 28-NOV-2000; 2000WO-US32378.
XX
XX PR 16-FEB-2000; 2000US-0182938.
XX PR 22-AUG-2000; 2000US-0226986.
XX
XX PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pitti RM;
PI Yan M;
XX
XX WPI; 2001-541628/60.

DR N-PSDB; AAD15904.
XX
PT Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
PT activity, for treating autoimmune disorders and cancer, comprises
PT exposing the cells to TALL-1 or APRIL polypeptide agonists or
PT antagonists -
XX
PS Claim 20; Fig 4; 160pp; English.
XX
CC The invention relates to methods of using one or more agonists or
CC antagonists to modulate the activity of the members of TNF (tumour
CC necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR)
CC e.g. TACI or BCMA. The method is useful for treating pathological
CC conditions or diseases associated with increased TALL-1 and APRIL
CC expression or activity. TALL-1 and APRIL antagonists are used to
CC block the interaction between APRIL and TALL-1 with TACI or BCMA.
CC They are useful for treating a mammal suffering from cancer such
CC as leukaemia, lymphoma, myeloma, cancers of lung and colon and
CC autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis,
CC psoriasis and lupus erythematosus. The present sequence is human
APRIL protein.

SO Sequence 250 AA;
Query Match 100.0%; Score 250; DB 22; Length 250;
Best Local Similarity 100.0%; Pred. No. 2e-234;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MPASSPFLAPKGPNGMGVPVREPALSVALWLSWGALGAVACAMALLTQOTELQSLRR 60
Db 1 MPASSPFLAPKGPNGMGVPVREPALSVALWLSWGALGAVACAMALLTQOTELQSLRR 60
OY 61 EVSRLOGTGSPSQNGEGYPMQSLPEQSSDALAEWENGERSRKRAVLTQOKKHSHVLHL 120
Db 61 EVSRLOGTGSPSQNGEGYPMQSLPEQSSDALAEWENGERSRKRAVLTQOKKHSHVLHL 120
OY 121 VPINATSKDSDVTEVMQPALRRGRLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQ 180
Db 121 VPINATSKDSDVTEVMQPALRRGRLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQ 180
OY 181 VVSREGQGRQETLFRICIRSMPSHPDRAYNSCYSAGVFHLHOGDILSVIIPRARAKNLSP 240
Db 181 VVSREGQGRQETLFRICIRSMPSHPDRAYNSCYSAGVFHLHOGDILSVIIPRARAKNLSP 240
OY 241 HGTFLGFVKL 250
Db 241 HGTFLGFVKL 250

RESULT 8
AAB62329
ID AAB62329 standard; protein; 250 AA.
XX
AC AAB62329;
XX
DT 29-JUN-2001 (first entry)
XX
DE Human TRDL-1alpha polypeptide.
XX
KW Tumour necrosis factor related death ligand-1gamma; TRDL-1gamma; TRDL;
KW cell death; apoptosis; human; TRDL-1alpha.
XX
OS Homo sapiens.
XX
PN WO200125256-A2.
XX
PD 12-APR-2001.
XX
PF 06-OCT-2000; 2000WO-US27868.
XX
PR 06-OCT-1999; 99US-0157913.
XX
PA (UTAH) UNIV UTAH RES FOUND.

XX Jones D, Manos E;
PI
XX
DR WPI; 2001-281728/29.
XX
PT Isolated and purified polynucleotide encoding human tumor necrosis
PT factor related death ligand (TRDL)-1 gamma useful for identifying
PT agents that inhibit or enhance TRDL-1 gamma mediated induction of
PT apoptosis -
XX
PS Disclosure; Fig 1; 39pp; English.
XX
CC The invention provides a human tumour necrosis factor related death
CC ligand-1gamma (TRDL-1gamma). The TRDL-1gamma polypeptide can be
CC expressed by standard recombinant methodology. TRDL-1gamma stimulates
CC Jurkat cell death. It is useful for identifying agents capable of
CC inhibiting or enhancing TRDL-1gamma mediated induction of apoptosis.
CC The present sequence represents a TRDL-1alpha polypeptide, used in
CC alignment studies.

SO Sequence 250 AA;
Query Match 100.0%; Score 250; DB 22; Length 250;
Best Local Similarity 100.0%; Pred. No. 2e-234;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MPASSPFLAPKGPNGMGVPVREPALSVALWLSWGALGAVACAMALLTQOTELQSLRR 60
Db 1 MPASSPFLAPKGPNGMGVPVREPALSVALWLSWGALGAVACAMALLTQOTELQSLRR 60
OY 61 EVSRLOGTGSPSQNGEGYPMQSLPEQSSDALAEWENGERSRKRAVLTQOKKHSHVLHL 120
Db 61 EVSRLOGTGSPSQNGEGYPMQSLPEQSSDALAEWENGERSRKRAVLTQOKKHSHVLHL 120
OY 121 VPINATSKDSDVTEVMQPALRRGRLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQ 180
Db 121 VPINATSKDSDVTEVMQPALRRGRLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQ 180
OY 181 VVSREGQGRQETLFRICIRSMPSHPDRAYNSCYSAGVFHLHOGDILSVIIPRARAKNLSP 240
Db 181 VVSREGQGRQETLFRICIRSMPSHPDRAYNSCYSAGVFHLHOGDILSVIIPRARAKNLSP 240
OY 241 HGTFLGFVKL 250
Db 241 HGTFLGFVKL 250

RESULT 9
AAY71981
ID AAY71981 standard; protein; 250 AA.
XX
AC AAY71981;
XX
DT 28-MAR-2001 (first entry)
XX
DE Human TNF and Apol-related Leucocyte-expressed Ligand 2/APRIL protein.
XX
KW Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
KW Tumour necrosis factor and Apol-related leucocyte expressed ligand;
KW therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
KW systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
KW thrombocytopenia purpura; acute rheumatic fever; myaesthesia gravis;
KW haemolytic anaemia; Grave's disease; Goodpasture's syndrome; TALL2/APRIL;
KW post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA;
KW B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.
XX
OS Homo sapiens.
XX
FH Key 28.48 Location/Qualifiers
FT Domain /label= Transmembrane_domain
FT Region 116..122
FT /label= Beta_strand

FT Region 138..140
/label= Beta_strand
FT Region 148..150
/label= Beta_strand
FT Region 153..156
/label= Beta_strand
FT Region 162..173
/label= Beta_strand
FT Region 187..192
/label= Beta_strand
FT Region 201..209
/label= Beta_strand
FT Region 210..217
/label= Beta_strand
FT Region 222..230
/label= Beta_strand
FT Region 243..250
/label= Beta_strand

WO200068378-A1.

16-NOV-2000.

05-MAY-2000; 2000WO-US12266.

06-MAY-1999; 99US-0132892.
01-MAY-2000; 2000US-0201012.

(NAJE-) NAT JEWISH MEDICAL & RES CENT.

Shu HS;

WPI; 2001-016094/02.

Isolated TALL-1 protein is used to identify compounds that regulate B lymphocyte proliferation, used to treat B lymphocyte associated autoimmune disorders -

Example 1; Fig 1a; 112pp; English.

CC The present invention relates to Tumour necrosis factor (TNF) and
CC Apol-related leucocyte expressed ligand 1 (TALL-1) nucleic acid
CC molecules, proteins (including homologues), and their antibodies. The
CC invention in particular relates to methods for regulating the
CC interaction between TALL-1 and TALL-1 receptors (BCMA referred as B cell
CC maturation factor) to regulate monocyte, macrophage and B lymphocyte
CC mediated immune responses. TALL-1 protein is useful for identifying
CC compounds that regulate B lymphocyte proliferation. It is also useful for
CC treating B lymphocyte associated autoimmune disorders like rheumatoid
CC arthritis, systemic lupus erythematosus (SLE), insulin dependent diabetes
CC mellitus, multiple sclerosis, myasthenia gravis, Grave's disease,
CC autoimmune haemolytic anaemia, autoimmune thrombocytopenia purpura,
CC Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever,
CC post-streptococcal glomerulonephritis, or polyarteritis nodosa.
CC The TALL-1 protein and its corresponding nucleic acid sequence are also
CC useful in diagnostic assays.
CC The present sequence is human Tumour necrosis factor (TNF) and
CC Apol-related leucocyte-expressed ligand 2 (TALL-2)/APRIL protein.
CC TALL-2/APRIL is encoded by the second TNF/FasL like gene. TALL2/APRIL
CC also belongs to the subfamily of TNF family of ligands.

XX Sequence 250 AA;

Query Match 100.0%; Score 250; DB 22; Length 250;
Best Local Similarity 100.0%; Pred. No. 2e-234;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPASSPFLAPKGPNGMGPVREPALSVALLMSGALGAVACAMALLTOQTQLQSLRR 60
DB 1 MPASSPFLAPKGPNGMGPVREPALSVALLMSGALGAVACAMALLTOQTQLQSLRR 60
QY 61 EVSRLQGTGPGSONGEGYPWQSLPEQSSDALFAWENGERSRKRRAVLTKOKKHSHVLHL 120

DB 61 EVSRLQGTGPGSONGEGYPWQSLPEQSSDALFAWENGERSRKRRAVLTKOKKHSHVLHL 120
QY 121 VPINATSKDSDVTEVMWQPALRGRGLQAOGCVRIQDAGVYLLYSQVLFQDVTFTMGQ 180
DB 121 VPINATSKDSDVTEVMWQPALRGRGLQAOGCVRIQDAGVYLLYSQVLFQDVTFTMGQ 180
QY 181 VVSREGQGRQETLFRICIRSMPSHPDRAYNSCYSAGVFHLHOGDILSVIIPRARKLNLSP 240
DB 181 VVSREGQGRQETLFRICIRSMPSHPDRAYNSCYSAGVFHLHOGDILSVIIPRARKLNLSP 240
QY 241 HGTFLGFVKL 250
DB 241 HGTFLGFVKL 250

RESULT 10
AAU99305
ID AAU99305 standard; Protein; 250 AA.

AC AAU99305;

DT 24-SEP-2002 (first entry)

DE Human tumour necrosis factor ligand (TNFL), TRASH protein #1.

KW Human; anti-inflammatory; immunomodulatory; TRASH; TNFL; TANGO 118;
KW tumour necrosis factor ligand; signal transduction; gene therapy;
KW diagnosis; immune response; inflammatory disorder;
KW differentiative disorder; developmental disorder.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Region 1..44
/note= "N-terminal signal transmembrane anchor
FT Region specifically claimed in claim 27 of the
FT Region specification"

FT Region 18..250
/note= "This region, TRASH protein #2, is specifically
FT Region claimed in claim 28 of the specification"
FT Region 46..250
/note= "This region, TRASH protein #3, is specifically
FT Region claimed in claim 28 of the specification"
FT Region 50..250
/note= "This region, TRASH protein #4, is specifically
FT Region claimed in claim 28 of the specification"

PN US2002055474-A1.

PD 09-MAY-2002.

PF 27-JAN-1998; 98US-0014348.

PR 27-JAN-1998; 98US-0014348.

PA (BUSF/) BUSFIELD S J.

PI Busfield SJ;

DR WPI; 2002-526818/56.

DR N-PSDB; ABK86985.

PT New nucleic acid encoding a protein designated TRASH is a member of the
PT tumor necrosis factor ligand superfamily of proteins and is useful to
PT detect and treat TRASH-associated disorders including immune and
PT inflammatory disorders -

PS Claim 28; Fig 1; 44pp; English.

CC The invention discloses an isolated nucleic acid encoding a novel tumour
CC necrosis factor ligand (TNFL), referred to as TRASH (not defined) (or
CC TANGO 118), protein. Members of the TNFL superfamily are involved in the
CC activation of a large array of cellular genes and of multiple signal

CC transduction pathways, kinases and transcription factors. The nucleic
CC acid and protein can be used in gene therapy, to identify compounds that
CC modulates TRASH activity, raise antibodies and treat, or diagnose,
CC disorders associated with aberrant TRASH activity or expression,
CC particularly an immune response or inflammatory disorder, or a
CC differential or developmental disorder. The sequence presented is the
CC human tumour necrosis factor ligand (TNFL), TRASH protein #1.

XX
SQ Sequence 250 AA;

Query Match 100.0%; Score 250; DB 23; Length 250;
Best Local Similarity 100.0%; Pred. No. 2e-234;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPASSPFLAPKGPNGMGPVREPALSVLWLSWGALGAVACAMALLTQOTELQSLRR 60
DB 1 MPASSPFLAPKGPNGMGPVREPALSVLWLSWGALGAVACAMALLTQOTELQSLRR 60
QY 61 EVSRLQGTGSPSONGEGYPMQSLPEQSSDALAEWENGERSRKRAVLTKQKKHSLVHL 120
DB 61 EVSRLQGTGSPSONGEGYPMQSLPEQSSDALAEWENGERSRKRAVLTKQKKHSLVHL 120
QY 121 VPINATSKDSDVTEVMQPALRRGRLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQ 180
DB 121 VPINATSKDSDVTEVMQPALRRGRLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQ 180
QY 181 VVSREGGROETLFRICIRSMPSHPDRAYNSCYAGVFHLHOGDILSVIIPRARAKNLSP 240
DB 181 VVSREGGROETLFRICIRSMPSHPDRAYNSCYAGVFHLHOGDILSVIIPRARAKNLSP 240
QY 241 HGTFLGFVKL 250
DB 241 HGTFLGFVKL 250

RESULT 11
ABB81486
ID ABB81486 standard; Protein; 250 AA.

AC ABB81486;
XX
DT 02-SEP-2002 (first entry)

DE Human ZTNF2 amino acid sequence SEQ ID NO:6.

KW Human; Ztnfr12; tumour necrosis factor receptor; cytostatic;
KW immunosuppressive; dermatological; antiinflammatory; antidiabetic;
KW neuroprotective; antirheumatic; antiarthritic; antiasthmatic;
KW nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;
KW autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;
KW multiple sclerosis; insulin dependent diabetes mellitus; asthma;
KW rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;
KW glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;
KW pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis;
KW light chain neuropathy; hypertension; large vessel disease;
KW graft-versus host disease; graft rejection; Crohn's disease.

XX Homo sapiens.

OS
PN WO200238766-A2.

XX
PD 16-MAY-2002.

XX
PF 05-NOV-2001; 2001WO-US47018.

XX
PR 07-NOV-2000; 2000US-246449P.

XX
PR 20-DEC-2000; 2000US-257131P.

XX
PR 28-JUN-2001; 2001US-301715P.

XX
PR 29-AUG-2001; 2001US-315565P.

XX
PA (ZYMO) ZYMOGENETICS INC.

XX
PI Gross JA, Xu W, Henne RM, Grant FJ;

XX
DR WPI; 2002-508212/54.

XX
PT Novel isolated human tumor necrosis factor receptor polypeptide, termed
PT ztnfr 12, useful for treating autoimmune disorders, emphysema, end
PT stage renal failure or renal disease and lymphoma
XX
PS Disclosure; Page 135; 154pp; English.

CC The present invention describes a human tumour necrosis factor receptor
CC designated ztnfr12 (I). (I) has cytostatic, immunosuppressive,
CC dermatological, antiinflammatory, neuroprotective, antidiabetic,
CC antirheumatic, antiarthritic, antiasthmatic, nephrotropic and hypotensive
CC activities, and can be used in gene therapy. (I) can be used for
CC inhibiting, in a mammal, the activity of a ligand that binds ztnfr12
CC (e.g. ZTNF4), for treating disorders and diseases associated with B
CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
CC inhibiting the proliferation of tumour cells. (I) is useful for treating
CC autoimmune disorders such as systemic lupus erythematosus, myasthenia
CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
CC leukaemia, nephritis, and pyelonephritis, and for treating renal
CC amyloidosis, hypertension, large vessel diseases, graft-versus host
CC disease, graft rejection and Crohn's disease. (I) is useful for
CC modulating the immune system, for regulating B cell responses and
CC development, for modulating development of other cells, antibody
CC production and cytokine production, and for modulating T and B cell
CC communication. The present sequence represents the human ZTNF2 protein
CC which is given in the exemplification of the present invention.

XX
SQ Sequence 250 AA;

Query Match 100.0%; Score 250; DB 23; Length 250;
Best Local Similarity 100.0%; Pred. No. 2e-234;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPASSPFLAPKGPNGMGPVREPALSVLWLSWGALGAVACAMALLTQOTELQSLRR 60
DB 1 MPASSPFLAPKGPNGMGPVREPALSVLWLSWGALGAVACAMALLTQOTELQSLRR 60
QY 61 EVSRLQGTGSPSONGEGYPMQSLPEQSSDALAEWENGERSRKRAVLTKQKKHSLVHL 120
DB 61 EVSRLQGTGSPSONGEGYPMQSLPEQSSDALAEWENGERSRKRAVLTKQKKHSLVHL 120
QY 121 VPINATSKDSDVTEVMQPALRRGRLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQ 180
DB 121 VPINATSKDSDVTEVMQPALRRGRLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQ 180
QY 181 VVSREGGROETLFRICIRSMPSHPDRAYNSCYAGVFHLHOGDILSVIIPRARAKNLSP 240
DB 181 VVSREGGROETLFRICIRSMPSHPDRAYNSCYAGVFHLHOGDILSVIIPRARAKNLSP 240
QY 241 HGTFLGFVKL 250
DB 241 HGTFLGFVKL 250

RESULT 12
ABP47228
ID ABP47228 standard; Protein; 250 AA.

XX
AC ABP47228;

XX
DT 19-AUG-2002 (first entry)

XX
DE Human Blys binding scFv VH CDR3 SEQ ID 3239.

KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;

KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US19110.
XX
PR 16-JUN-2000; 2000US-212210P.
PR 17-OCT-2000; 2000US-240816P.
PR 16-MAR-2001; 2001US-276248P.
PR 21-MAR-2001; 2001US-277379P.
PR 25-MAY-2001; 2001US-293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
DR Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
XX
PT Antibodies against B lymphocyte stimulating polypeptides, useful for
XX the diagnosis and treatment of cancers and immune disorders -
XX
PS Disclosure; Page 3147-3148; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method
CC of the invention.
XX
XX Sequence 250 AA;
Query Match 100.0%; Score 250; DB 23; Length 250;
Best Local Similarity 100.0%; Pred. No. 2e-234;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPASSPFLAPKPGPGNMGGPVREPALSVLWLSWGALGAVACAMALLTQOTELQSLRR 60
Db 1 MPASSPFLAPKPGPGNMGGPVREPALSVLWLSWGALGAVACAMALLTQOTELQSLRR 60
QY 61 EVSRLQGTGSPSONGEGYPWQSLPEQSSDALFAWENGERSRKRAVLTKOKKHSHVLHL 120
Db 61 EVSRLQGTGSPSONGEGYPWQSLPEQSSDALFAWENGERSRKRAVLTKOKKHSHVLHL 120
QY 121 VPINATSKDDSDVTEVMQPALRRGRGQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQ 180
Db 121 VPINATSKDDSDVTEVMQPALRRGRGQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQ 180
QY 181 VVSREGGROETLFRCTIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIPRAKLNLS 240
Db 181 VVSREGGROETLFRCTIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIPRAKLNLS 240
QY 241 HGTFLGFVKL 250
Db 241 HGTFLGFVKL 250

RESULT 13
AAU79155
ID AAU79155 standard; Protein; 250 AA.
XX
AC AAU79155;
XX
DT 02-JUL-2002 (first entry)
XX
DE Human APRIL (a proliferation-inducing ligand) protein #2.
XX
KW Human; Neutrokin-alpha; antibody; immunogen; B-cell cancer;
KW autoimmune disease; Sjogren's syndrome; systemic lupus erythematosus;
KW rheumatoid arthritis; chronic lymphocytic leukaemia; multiple myeloma;
KW Hodgkin's lymphoma; non-Hodgkin's lymphoma; hypergammaglobulinemia;
KW APRIL; a proliferation-inducing ligand.
XX
OS Homo sapiens.
XX
PN WO200218620-A2.
XX
PD 07-MAR-2002.
XX
PF 15-AUG-2001; 2001WO-US25549.
XX
PR 15-AUG-2000; 2000US-225628P.
PR 23-AUG-2000; 2000US-227008P.
PR 22-SEP-2000; 2000US-234338P.
PR 17-OCT-2000; 2000US-240806P.
PR 30-NOV-2000; 2000US-250020P.
PR 06-MAR-2001; 2001US-276248P.
PR 25-MAY-2001; 2001US-293499P.
PR 07-JUN-2001; 2001US-296122P.
PR 13-JUL-2001; 2001US-304809P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Yu G, Ebner R, Ni J, Rosen CA, Ullrich S;
XX WPI; 2002-304259/34.
XX
PT An isolated antibody or portion that specifically binds to a protein
PT useful in the treatment of diseases such as hypergammaglobulinemia and
XX cancer -
XX
PS Claim 1; Page 481-482; 482pp; English.
XX
CC The present invention relates to a new antibody, or portion, that
CC specifically binds to a protein which has a 285 or 250 amino acid
CC sequence as fully defined in the specification. The antibody of the
CC invention is useful in treating a disease or disorder such as cancer,
CC especially B-cell cancer, autoimmune diseases such as Sjogren's
CC syndrome, systemic lupus erythematosus, rheumatoid arthritis, chronic
CC lymphocytic leukaemia, multiple myeloma, Hodgkin's lymphoma,
CC non-Hodgkin's lymphoma or hypergammaglobulinemia, or in diagnosing a
CC disease or disorder comprising assaying expression of Neutrokin-alpha
CC and APRIL (a proliferation-inducing ligand) in cells or body fluids using
CC antibodies and comparing the Neutrokin-alpha and APRIL expression level
CC with a standard Neutrokin-alpha and APRIL expression level, whereby an
CC increase or decrease in the assayed Neutrokin-alpha and APRIL expression
CC level compared to the standard levels is indicative of a disease or
CC disorder. The present amino acid sequence represents the human APRIL
CC protein #2 of the invention.
XX
XX Sequence 250 AA;
Query Match 100.0%; Score 250; DB 23; Length 250;
Best Local Similarity 100.0%; Pred. No. 2e-234;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPASSPFLAPKPGPGNMGGPVREPALSVLWLSWGALGAVACAMALLTQOTELQSLRR 60
Db 1 MPASSPFLAPKPGPGNMGGPVREPALSVLWLSWGALGAVACAMALLTQOTELQSLRR 60

OY 61 EVSRLOGTGSPSQNGEGYPWQSLPEQSSDALAEWNGERSRKRAVLTKOKKQHSVLHL 120
DB 61 EVSRLOGTGSPSQNGEGYPWQSLPEQSSDALAEWNGERSRKRAVLTKOKKQHSVLHL 120
OY 121 VPINATSKDSDVTEVMWQPALRRGRGLQAQGYVRIQDAGVYLLYSQVLFQDVTFTMGQ 180
DB 121 VPINATSKDSDVTEVMWQPALRRGRGLQAQGYVRIQDAGVYLLYSQVLFQDVTFTMGQ 180
OY 181 VVSREGQGRQETLFRFCIRSMPSHPDRAYNSCYSAGVFHLHOGDILSVIIPARAKLNLS 240
DB 181 VVSREGQGRQETLFRFCIRSMPSHPDRAYNSCYSAGVFHLHOGDILSVIIPARAKLNLS 240
OY 241 HGTFLGFVKL 250
DB 241 HGTFLGFVKL 250
RESULT 14
AAV28836
AAV28836 standard; Protein; 247 AA.
AAV28836;
17-JAN-2000 (first entry)
Human TNF-related death ligand-14.
Tumour necrosis factor-related death ligand-14; TRDL-14; cytokine;
TNF alpha; Fas ligand; FasL; TNF-related apoptosis-inducing ligand;
TRAIL; cellular apoptosis; transcription factor; NF kappa B; cancer;
autoimmune disease; viral infection; antagonist; AIDS; probe; primer;
neurodegenerative disease; myelodysplastic disease; ischaemic injury;
chromosome localisation; antibody.
Homo sapiens.
Key Location/Qualifiers
Domain 1..23
/label= N-terminal_cytoplasmic_domain
Domain 24..52
/label= Transmembrane_domain
Domain 53..247
/label= C-terminal_extracellular_domain
W09950416-A1.
07-OCT-1999.
21-SEP-1998; 98WO-US18506.
30-SEP-1997; 97US-0060475.
(PHAA) PHARMACIA & UPJOHN CO.
Bienkowski MJ, Jones DA, Mills CJ;
WPI: 1999-610854/52.
N-PSDB; AAX90911.
New nucleic acid used for promotion or inhibition of apoptosis, e.g.
for treating cancer -
Claim 1; Fig 4; 70pp; English.
The present sequence is tumour necrosis factor (TNF)-related death
ligand-14 (TRDL-14), that belongs to cytokine family. It shows 17%, 17%
and 12% sequence homology to the C-terminal domains of TNF alpha, Fas
ligand (FasL) and TNF-related apoptosis-inducing ligand (TRAIL)
respectively. It can activate cellular apoptosis and transcription factor
NF kappa B and can be used for treating conditions associated with
inadequate levels of apoptosis, like cancer, autoimmune disease and viral
infections. TRDL antagonist can be used to reduce apoptosis levels in

CC conditions like, AIDS, neurodegenerative diseases, myelodysplastic
CC disease and ischaemic injury. TRDL gene can be used for chromosome
CC localisation and as probe or primer for detecting TRDL nucleic acid or
CC cells that express TRDL. Antibodies generated against TRDL are useful for
CC detecting TRDL expression.
XX
SQ Sequence 247 AA;
Query Match 98.4%; Score 246; DB 20; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.6e-230;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MPASSPFLAPKCPGPMGVPREBALSVALWLSGVALGAVACAMALLTQOTELQSLRR 60
DB 1 MPASSPFLAPKCPGPMGVPREBALSVALWLSGVALGAVACAMALLTQOTELQSLRR 60
OY 61 EVSRLOGTGSPSQNGEGYPWQSLPEQSSDALAEWNGERSRKRAVLTKOKKQHSVLHL 120
DB 61 EVSRLOGTGSPSQNGEGYPWQSLPEQSSDALAEWNGERSRKRAVLTKOKKQHSVLHL 120
OY 121 VPINATSKDSDVTEVMWQPALRRGRGLQAQGYVRIQDAGVYLLYSQVLFQDVTFTMGQ 180
DB 121 VPINATSKDSDVTEVMWQPALRRGRGLQAQGYVRIQDAGVYLLYSQVLFQDVTFTMGQ 180
OY 181 VVSREGQGRQETLFRFCIRSMPSHPDRAYNSCYSAGVFHLHOGDILSVIIPARAKLNLS 240
DB 181 VVSREGQGRQETLFRFCIRSMPSHPDRAYNSCYSAGVFHLHOGDILSVIIPARAKLNLS 240
OY 241 HGTFLG 246
DB 241 HGTFLG 246
RESULT 15
AAB62327
ID AAB62327 standard; Protein; 247 AA.
AAB62327;
29-JUN-2001 (first entry)
Human TRDL-1gamma polypeptide.
Tumour necrosis factor related death ligand-1gamma; TRDL-1gamma; TRDL;
cell death; apoptosis; human.
XX
OS Homo sapiens.
XX
PN W0200125256-A2.
XX
PD 12-APR-2001.
XX
PF 06-OCT-2000; 2000WO-US27868.
XX
PR 06-OCT-1999; 99US-0157913.
XX
PA (UTAH) UNIV UTAH RES FOUND.
XX
PI Jones D, Manos E;
XX
DR WPI: 2001-281728/29.
DR N-PSDB; AAF57680.
XX
PT Isolated and purified polynucleotide encoding human tumor necrosis
PT factor related death ligand (TRDL)-1 gamma useful for identifying
PT agents that inhibit or enhance TRDL-1 gamma mediated induction of
PT apoptosis -
XX
PS Claim 1; Page 34-36; 39pp; English.
XX This represents a human tumour necrosis factor related death
CC ligand-1gamma (TRDL-1gamma). The TRDL-1gamma polypeptide can be
CC expressed by standard recombinant methodology. TRDL-1gamma stimulates

CC Jurkat cell death. It is useful for identifying agents capable of
CC inhibiting or enhancing TRDL-1gamma mediated induction of apoptosis.
XX
SQ Sequence 247 AA;

Query Match 98.4%; Score 246; DB 22; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.6e-230;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPASSPFLAPKGPNGGVPREPALSVLWLSWGALGAVACAMALLTQOTELQSLRR 60
DB 1 MPASSPFLAPKGPNGGVPREPALSVLWLSWGALGAVACAMALLTQOTELQSLRR 60
QY 61 EVSRLOGTGSPSQNGEGYPMQSLPEQSSDALLEAWENGERSRKRRAVLTQOKKQSHVHL 120
DB 61 EVSRLOGTGSPSQNGEGYPMQSLPEQSSDALLEAWENGERSRKRRAVLTQOKKQSHVHL 120
QY 121 VPINATSKDDSDVTEVMQPALRRGRGLQAGYGVRIQDAGVYLLYSQVLFQDVTFTMGQ 180
DB 121 VPINATSKDDSDVTEVMQPALRRGRGLQAGYGVRIQDAGVYLLYSQVLFQDVTFTMGQ 180
DB 181 VVSREGGROETLFRCTIRSMPSHPDRAYNSCYSGVFFHLHOGDILSVIIPRARAKLNSP 240
DB 181 VVSREGGROETLFRCTIRSMPSHPDRAYNSCYSGVFFHLHOGDILSVIIPRARAKLNSP 240
QY 241 HGTFLG 246
DB 241 HGTFLG 246

RESULT 16

ID AAY22225 standard; Protein; 205 AA.

XX AC AAY22225;

DT 16-SEP-1999 (first entry)

DE Human TNFL2 protein sequence.

XX TNFL1; human; TNFR superfamily; tumour necrosis factor ligand; TNF;
KW tumour necrosis factor receptor; TNFR superfamily; cell proliferation;
KW cell differentiation; cytokine production; immunoglobulin; hyperplasia;
KW apoptosis inducer; activated T cell; autoimmune disease; inhibitor;
KW myasthenia gravis; insulin-dependent diabetes mellitus; endotoxin shock;
KW rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus;
KW tumour; proliferative disorder; neoplasia; dysplasia; immunocompetence;
KW lymphoid organogenesis; bacterial resistance; contact hypersensitivity;
KW delayed type sensitivity; therapy.

XX Homo sapiens.

PN WO9933980-A2.

PD 08-JUL-1999.

PF 22-DEC-1998; 98WO-US27474.

PR 16-DEC-1998; 98US-0212270.

PR 30-DEC-1997; 97US-0068959.

PA (CHIR) CHIRON CORP.

PI Kassam A, Lamson G, Pot D, Tribouley C;

DR WPI; 1999-405508/34.

DR N-PSDB; AAX84624.

PT New tumour necrosis factor ligands, useful for induction of cell
PT death and/or proliferation of cells
XX
PS Claim 13; Page 63; 69pp; English.
XX

CC This sequence is the tumour necrosis factor (TNF) ligand family
CC protein of the invention, designated TNFL2. The TNFL proteins play
CC regulatory roles in cell proliferation and/or differentiation, e.g. they
CC can induce production of cytokines, immunoglobulins, etc. A variety of
CC diseases can be treated by modulating the activity of TNFL proteins,
CC e.g. they can induce apoptosis of activated T cells but rescue resting
CC T cell from apoptosis. TNFL polypeptides can therefore be used to treat
CC autoimmune diseases, such as myasthenia gravis, insulin-dependent
CC diabetes mellitus, rheumatoid arthritis, multiple sclerosis, and systemic
CC lupus erythematosus. TNFL proteins also have tumour stimulating
CC properties, so tumours can be treated by inhibiting the expression or
CC activity of TNFL. Other proliferative disorders, such as neoplasias,
CC dysplasias, and hyperplasia can also be treated using TNFL inhibitors.
CC The TNFL polypeptides and polynucleotides can also be used to enhance or
CC decrease TNF activity, thus providing therapeutic benefits such as
CC induction of cell death, lymphoid organogenesis, or host bacterial
CC resistance, and inhibition of endotoxin shock, contact hypersensitivity,
CC delayed type sensitivity or immunocompetence of a transplant recipient.
CC Tumour necrosis factor (TNF) and its receptors play a major role in host
CC defence and immunosurveillance. As such, there is a need to identify new
CC members of TNFR families. This invention provides this need.

SQ Sequence 205 AA;

Query Match 80.8%; Score 202; DB 20; Length 205;
Best Local Similarity 100.0%; Pred. No. 7.1e-188;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 LTQOTELQSLRREVSRLOGTGSPSQNGEGYPMQSLPEQSSDALLEAWENGERSRKRRAVLT 108
DB 4 LTQOTELQSLRREVSRLOGTGSPSQNGEGYPMQSLPEQSSDALLEAWENGERSRKRRAVLT 63

QY 109 QKOKKQSHVHLVPINATSKDDSDVTEVMQPALRRGRGLQAGYGVRIQDAGVYLLYSQ 168
DB 64 QKOKKQSHVHLVPINATSKDDSDVTEVMQPALRRGRGLQAGYGVRIQDAGVYLLYSQ 123

QY 169 VLFQDVTFTMGQVVSREGGROETLFRCTIRSMPSHPDRAYNSCYSGVFFHLHOGDILSVI 228
DB 124 VLFQDVTFTMGQVVSREGGROETLFRCTIRSMPSHPDRAYNSCYSGVFFHLHOGDILSVI 183

QY 229 IPRARAKLNSPHGTFLGFKL 250
DB 184 IPRARAKLNSPHGTFLGFKL 205

RESULT 17

ID AAU99508 standard; Protein; 233 AA.

XX AC AAU99508;

DT 07-OCT-2002 (first entry)

DE Human tumour necrosis factor (TNF) delta #1.

XX Human; tumour necrosis factor; TNF delta; pulmonary system disorder;
KW immunoglobulin production; B-cell proliferation; immune system disorder;
KW autoimmune disease; cancer; lymphoproliferative disorder; pain;
KW microbial infection; parasitic infection; bone disease; atherosclerosis;
KW cardiovascular disorder; neurodegenerative disease; wound healing;
KW graft versus host disease; haematopoietic cell disorder; nephritis;
KW inflammatory disorder; mucous membrane disorder; dermatological;
KW immunosuppressive; cytostatic.

XX Homo sapiens.

PN US2002064829-A1.

PD 30-MAY-2002.

PF 14-JUN-2001; 2001US-0879919.

PR 14-MAR-1996; 96US-016812P.

PR 15-JUN-2000; 2000US-211537P.
PR 23-OCT-2000; 2000US-241952P.
PR 13-DEC-2000; 2000US-254875P.
PR 16-MAR-2001; 2001US-276248P.
PR 23-MAR-2001; 2001US-277978P.
PR 25-MAY-2001; 2001US-293499P.
PR 12-MAR-1997; 97US-0815783.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Yu G, Ni J, Gentz RL, Dillon PJ;
XX
DR WPI; 2002-556722/59.
DR N-PSDB; ABK88683.
XX
PT Novel human multimeric tumour necrosis factor delta or epsilon protein
PT useful for treating disease or disorder of immune system such as
PT autoimmune disease, immunodeficiency, or cancer of immune system -
XX
XX Claim 1; Fig 1; 143pp; English.
CC The present invention relates to the isolation of human tumour necrosis
CC factor (TNF) delta and TNF epsilon proteins, and the polynucleotide
CC sequences encoding them. The proteins are useful for modulating
CC immunoglobulin production or for modulating proliferation of B-cells.
CC The sequences of the invention are useful for treating diseases or
CC disorders of the immune system. Such disorders include autoimmune
CC diseases (e.g. systemic lupus erythematosus (SLE), acquired
CC immunodeficiency syndrome (AIDS)), cancers of the immune system
CC (e.g. chronic lymphocytic leukaemia (CLL), multiple myeloma,
CC non-Hodgkin's lymphoma or Hodgkin's disease), lymphoproliferative
CC disorders, microbial infections (e.g. viral, bacterial), parasitic
CC infections, nephritis, bone disease (e.g. osteoporosis), atherosclerosis,
CC pain, cardiovascular disorders (e.g. myocardial infarction, stroke),
CC neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's
CC disease), graft versus host disease, wound healing, haematopoietic cell
CC disorders (e.g. anaemia), inflammatory disorders (e.g. asthma),
CC diseases or disorders associated with various mucous membranes of the
CC body (e.g. mucositis), and disorders of the pulmonary system. The
CC proteins are also useful as a vaccine adjuvant that enhances immune
CC responsiveness to specific antigens. The present sequence represents
CC human TNF delta #1.
XX
SQ Sequence 233 AA;
Query Match 73.2%; Score 183; DB 23; Length 233;
Best Local Similarity 100.0%; Pred. No. 2.3e-169;
Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX
DE Tumour necrosis factor delta (TNF-delta), splicing variant #1.
XX
XX
KW Tumour necrosis factor delta; TNF-delta; cytostatic; arteriosclerosis;
KW analgesic; cerebroprotective; neurotrophic; neuroprotective; hepatotropic;
KW immunoglobulin production; B cell proliferation; immunosuppressive;
KW HIV; human immunodeficiency virus; autoimmune disease; immunodeficiency;
KW Sjogren's syndrome; systemic lupus erythematosus; Hodgkin's disease;
KW common variable immunodeficiency; CVID; non-Hodgkin's lymphoma; AIDS;
KW acquired immunodeficiency virus; cancer; multiple myeloma; CLL;
KW chronic lymphocytic leukaemia; lymphoproliferative disorder;
KW bacterial infection; viral infection; osteoporosis; atherosclerosis;
KW pain; cardiovascular disorder; stroke; allergy; Alzheimer's disease;
KW neurodegenerative disease; inflammation; liver disease; cirrhosis;
KW cardiomyopathy; diabetes; asthma; psoriasis; glomerulonephritis;
KW ulcerative colitis; angiogenesis; septic shock; wound healing.
XX
OS Homo sapiens.
XX
FH Key
FH Peptide
FT Location/Qualifiers
FT 1..87
FT /label= Signal_peptide
FT 88..233
FT /label= Mature_TNF-delta
FT /note= "Tumour necrosis factor"
FT /note= "Specifically claimed in claim 1"
FT 39..233
FT /note= "Specifically claimed in claim 1"
FT 59..66
FT /label= Conserved_domain_I
FT /note= "Region of high identity between TNF-delta
FT and TNF-epsilon"
FT 96..104
FT /label= Conserved_domain_II
FT /note= "Region of high identity between TNF-delta
FT and TNF-epsilon"
FT 112..121
FT /label= Conserved_domain_III
FT /note= "Region of high identity between TNF-delta
FT and TNF-epsilon"
FT 126..139
FT /label= Conserved_domain_IV
FT /note= "Region of high identity between TNF-delta
FT and TNF-epsilon"
FT 138..154
FT /note= "TNF family signature sequence"
FT 143..154
FT /label= Conserved_domain_V
FT /note= "Region of high identity between TNF-delta
FT and TNF-epsilon"
FT 166..176
FT /label= Conserved_domain_VI
FT /note= "Region of high identity between TNF-delta
FT and TNF-epsilon"
FT 178..183
FT /label= Conserved_domain_VII
FT /note= "Region of high identity between TNF-delta
FT and TNF-epsilon"
FT 191..195
FT /label= Conserved_domain_VIII
FT /note= "Region of high identity between TNF-delta
FT and TNF-epsilon"
FT 198..209
FT /label= Conserved_domain_IX
FT /note= "Region of high identity between TNF-delta
FT and TNF-epsilon"
FT 229..233
FT /label= Conserved_domain_XI
FT /note= "Region of high identity between TNF-delta
FT and TNF-epsilon"
XX
PN WO200196528-A2.
XX

PD 20-DEC-2001.
XX
PF 14-JUN-2001; 2001WO-US19026.
XX
PR 15-JUN-2000; 2000US-211537P.
PR 23-OCT-2000; 2000US-241952P.
PR 13-DEC-2000; 2000US-254875P.
PR 16-MAR-2001; 2001US-276248P.
PR 23-MAR-2001; 2001US-277978P.
PR 25-MAY-2001; 2001US-293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Yu G, Ni J, Gentz RL, Dillon PJ, Hilbert D;
XX
DR WPI; 2002-130727/17.
DR N-PSDB; ABK13401.
XX
PT Novel multimeric human tumour necrosis factor delta or epsilon protein
useful for treating cancer, immune system disorders, infection,
cardiovascular disorders, liver disease, cardiomyopathy, diabetes and
psoriasis -
XX
PS Claim 1; Fig 1A-B; 344bp; English.
XX
CC The invention describes a multimeric human tumour necrosis factor (TNF)
delta or epsilon protein (I). (I) or a composition containing them (II)
are useful for modulating immunoglobulin production or proliferation of B
cells. (I) or (II) is useful: for treating a disease or disorder of the
immune system, preferably an autoimmune disease (e.g. Sjogren's syndrome,
systemic lupus erythematosus or common variable immunodeficiency (CVID));
an immunodeficiency e.g. acquired immunodeficiency syndrome (AIDS);
cancer of the immune system (e.g. Hodgkin's disease, non-Hodgkin's
lymphoma, multiple myeloma and chronic lymphocytic leukaemia (CLL)); in
the diagnosis and treatment or prevention of cancer, lymphoproliferative
disorder, bacterial and viral infections, osteoporosis, atherosclerosis,
pain, cardiovascular disorders (e.g. stroke), allergy, inflammation,
neurodegenerative disease (e.g. Alzheimer's disease), liver disease (e.g.
cirrhosis), cardiomyopathy, diabetes, asthma, psoriasis, septic shock,
glomerulonephritis, ulcerative colitis, arteriosclerosis; for promoting
angiogenesis and wound healing; as a diagnostic research reagent; as an
agent to target and kill cells expressing a TNFdelta and/or TNFepsilon
receptor; in apoptosis of transformed cell lines; mediation of cell
activation and proliferation; and as an immunogen to produce (II). (II)
is useful to purify, detect and target (I), for measuring levels of (I)
in biological samples, for immunophenotyping samples, and to treat,
inhibit or prevent diseases and disorders associated with aberrant
expression and/or activity of (I). This is the amino acid sequence of
human tumour necrosis factor delta (TNF-delta) splicing variant #1,
described in the method of the invention.
XX
SQ Sequence 233 AA;
Query Match 73.2%; Score 183; DB 23; Length 233;
Best Local Similarity 100.0%; Pred. No. 2.3e-169;
Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 68 TGGPSQNGEGYPMQSLPEQSSDALFAWENGERSRKRRAVLTKOKKHSHLVLPINATS 127
Db 51 TGGPSQNGEGYPMQSLPEQSSDALFAWENGERSRKRRAVLTKOKKHSHLVLPINATS 110
QY 128 KDDSDVTEVMQPALRRGRGLAQGYGVRIQDAGVYLLYSQVLPQDVTFTMGQVVSREGQ 187
Db 111 KDDSDVTEVMQPALRRGRGLAQGYGVRIQDAGVYLLYSQVLPQDVTFTMGQVVSREGQ 170
QY 188 GROETLFRICRISMPSPHPRAYNSCYSAGVPHLHOGDILSVIIPRARAKLNLSPHGTFLGF 247
Db 171 GROETLFRICRISMPSPHPRAYNSCYSAGVPHLHOGDILSVIIPRARAKLNLSPHGTFLGF 230
QY 248 VKL 250
Db 231 VKL 233

RESULT 19
AA05745
ID AAY05745 standard; Protein; 250 AA.
XX
AC AAY05745;
XX
DT 19-JUL-1999 (first entry)
XX
DE Tumour necrosis factor receptor ligand TL3.
XX
KW Tumour necrosis factor receptor ligand; TL3; agonist;
KW antagonist; screening; human; cancer; AIDS; Alzheimer's disease;
KW inflammation; arthritis; septicemia; autoimmune disease;
KW psoriasis; inflammatory bowel disease; transplant rejection;
KW graft versus host disease; infection; stroke; ischaemia;
KW acute respiratory disease syndrome; restenosis; brain injury;
KW bone disease; atherosclerosis; therapy.
XX
OS Homo sapiens.
XX
PN EP911633-A1.
XX
PD 28-APR-1999.
XX
PF 02-OCT-1998; 98EP-0203332.
XX
PR 08-OCT-1997; 97US-0061334.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI McDonnell PC, Young PR, Zou J;
XX
DR WPI; 1999-246560/21.
DR N-PSDB; AAX25380.
XX
PT Identifying agonists and antagonists of tumor necrosis factor
PT related receptors TR1, TR3 and TR5, and of ligand TL3, useful for
PT treatment of cancer, AIDS, Alzheimer's disease, bone disease etc
XX
PS Disclosure; Page 14-15; 23pp; English.
XX
CC The present sequence represents tumour necrosis factor receptor
CC (TNFR) ligand TL3, which acts as a ligand for TNFRs TR1, TR3 and
CC TR5 (see AAY05742-44). TR1, TR3, TR5 and TL3 are used in claimed
CC methods of identifying agonists and antagonists, i.e. compounds
CC that bind to the receptors or ligand, and which activate (agonist)
CC or inhibit activation of (antagonists) TR1, TR3, TR5 or TL3. A
CC screening kit for identifying agonists, antagonists, ligands,
CC receptors, substrates, enzymes etc. for TR1, TR3, TR5 or TL3
CC polypeptides is provided. The agonists and antagonists are
CC useful for treatment of chronic and acute inflammation, arthritis,
CC septicemia, autoimmune disease e.g. inflammatory bowel disease,
CC psoriasis, transplant rejection, graft versus host disease,
CC infection, stroke, ischaemia, acute respiratory disease syndrome,
CC restenosis, brain injury, AIDS, bone diseases, cancer (e.g.
CC lymphoproliferative disorders), atherosclerosis and Alzheimer's
CC disease, etc., caused by imbalance of TR1, TR3, TR5 or TL3.
XX
SQ Sequence 250 AA;
Query Match 73.2%; Score 183; DB 20; Length 250;
Best Local Similarity 100.0%; Pred. No. 2.4e-169;
Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 68 TGGPSQNGEGYPMQSLPEQSSDALFAWENGERSRKRRAVLTKOKKHSHLVLPINATS 127
Db 68 TGGPSQNGEGYPMQSLPEQSSDALFAWENGERSRKRRAVLTKOKKHSHLVLPINATS 127
QY 128 KDDSDVTEVMQPALRRGRGLAQGYGVRIQDAGVYLLYSQVLPQDVTFTMGQVVSREGQ 187
Db 128 KDDSDVTEVMQPALRRGRGLAQGYGVRIQDAGVYLLYSQVLPQDVTFTMGQVVSREGQ 187

QY 188 GROETLFRICRSMPSHPDRAYNSCYSAGVFLHQGDILSVIIPRARA KLNLSPHGTFLGF 247
 |||
 Db 188 GROETLFRICRSMPSHPDRAYNSCYSAGVFLHQGDILSVIIPRARA KLNLSPHGTFLGF 247

QY 248 VKL 250
 |||
 Db 248 VKL 250

RESULT 20
 AAU99510
 ID AAU99510 standard; Protein; 250 AA.

XX AAU99510;
 AC
 DT 07-OCT-2002 (first entry)

DE Human tumour necrosis factor (TNF) delta #2.
 XX
 KM Human; tumour necrosis factor; TNF delta; pulmonary system disorder;
 KM immunoglobulin production; B-cell proliferation; immune system disorder;
 KM autoimmune disease; cancer; lymphoproliferative disorder; pain;
 KM microbial infection; parasitic infection; bone disease; atherosclerosis;
 KM cardiovascular disorder; neurodegenerative disease; wound healing;
 KM graft versus host disease; haematopoietic cell disorder; nephritis;
 KM inflammatory disorder; mucous membrane disorder; dermatological;
 KM immunosuppressive; cytostatic.

OS Homo sapiens.
 XX
 PN US2002064829-A1.
 PD 30-MAY-2002.
 XX
 PF 14-JUN-2001; 2001US-0879919.
 XX
 PR 14-MAR-1996; 96US-016812P.
 PR 15-JUN-2000; 2000US-211537P.
 PR 23-OCT-2000; 2000US-241952P.
 PR 13-DEC-2000; 2000US-254875P.
 PR 16-MAR-2001; 2001US-276248P.
 PR 23-MAR-2001; 2001US-277978P.
 PR 25-MAY-2001; 2001US-293499P.
 PR 12-MAR-1997; 97US-0815783.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Yu G, Ni J, Gentz RL, Dillon PJ;
 DR N-PSDB; ABK88683.
 XX
 PT Novel human multimeric tumour necrosis factor delta or epsilon protein
 PT useful for treating disease or disorder of immune system such as
 PT autoimmune disease, immunodeficiency, or cancer of immune system -
 XX
 PS Claim 1; Fig 6; 143pp; English.
 XX
 CC The present invention relates to the isolation of human tumour necrosis
 CC factor (TNF) delta and TNF epsilon proteins, and the polynucleotide
 CC sequences encoding them. The proteins are useful for modulating
 CC immunoglobulin production or for modulating proliferation of B-cells.
 CC The sequences of the invention are useful for treating diseases or
 CC disorders of the immune system. Such disorders include autoimmune
 CC diseases (e.g. systemic lupus erythematosus (SLE), acquired
 CC immunodeficiency syndrome (AIDS)), cancers of the immune system
 CC (e.g. chronic lymphocytic leukaemia (CLL), multiple myeloma,
 CC non-Hodgkin's lymphoma or Hodgkin's disease), lymphoproliferative
 CC disorders, microbial infections (e.g. viral, bacterial), parasitic
 CC infections, nephritis, bone disease (e.g. osteoporosis), atherosclerosis,
 CC pain, cardiovascular disorders (e.g. myocardial infarction, stroke),
 CC neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's
 CC disease), graft versus host disease, wound healing, haematopoietic cell

CC disorders (e.g. anaemia), inflammatory disorders (e.g. asthma),
 CC diseases or disorders associated with various mucous membranes of the
 CC body (e.g. mucositis), and disorders of the pulmonary system. The
 CC proteins are also useful as a vaccine adjuvant that enhances immune
 CC responsiveness to specific antigens. The present sequence represents
 CC human TNF delta #2.
 XX
 SQ Sequence 250 AA;

Query Match 73.2%; Score 183; DB 23; Length 250;
 Best Local Similarity 100.0%; Pred. No. 2.4e-169;
 Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 TGSPSONGEGYPWQSLPEQSSDALEAWENGERSRKRRAVLTKQKKQSHVLHVPINATS 127
 |||
 Db 68 TGSPSONGEGYPWQSLPEQSSDALEAWENGERSRKRRAVLTKQKKQSHVLHVPINATS 127

QY 128 KDDSDVTEVMWQPALRRGRGLQAGYGVRIQDAGVYLLYSQVLPQDVTFTMGQVVSREQQ 187
 |||
 Db 128 KDDSDVTEVMWQPALRRGRGLQAGYGVRIQDAGVYLLYSQVLPQDVTFTMGQVVSREQQ 187

QY 188 GROETLFRICRSMPSHPDRAYNSCYSAGVFLHQGDILSVIIPRARA KLNLSPHGTFLGF 247
 |||
 Db 188 GROETLFRICRSMPSHPDRAYNSCYSAGVFLHQGDILSVIIPRARA KLNLSPHGTFLGF 247

QY 248 VKL 250
 |||
 Db 248 VKL 250

RESULT 21
 AAU75406
 ID AAU75406 standard; Protein; 250 AA.

XX AAU75406;
 AC
 DT 09-APR-2002 (first entry)

DE Tumour necrosis factor delta (TNF-delta), splicing variant #2.
 XX
 KM Tumour necrosis factor delta; TNF-delta; cytostatic; arteriosclerosis;
 KM analgesic; cerebroprotective; neurotrophic; neuroprotective; hepatotropic;
 KM immunoglobulin production; B cell proliferation; immunosuppressive;
 KM HIV; human immunodeficiency virus; autoimmune disease; immunodeficiency;
 KM Sjogren's syndrome; systemic lupus erythematosus; Hodgkin's disease;
 KM common variable immunodeficiency; CVID; cancer; non-Hodgkin's lymphoma;
 KM AIDS; acquired immunodeficiency virus; multiple myeloma; CLL;
 KM chronic lymphocytic leukaemia; atherosclerosis; bacterial infection;
 KM lymphoproliferative disorder; viral infection; osteoporosis; pain;
 KM cardiovascular disorder; stroke; allergy; Alzheimer's disease;
 KM neurodegenerative disease; inflammation; liver disease; cirrhosis;
 KM cardiomyopathy; diabetes; psoriasis; glomerulonephritis;
 KM ulcerative colitis; angiogenesis; septic shock; wound healing.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT Peptide
 FT Protein
 FT Domain
 FT Domain
 FT Domain

Location/Qualifiers
 1..104
 /label= Signal_peptide
 105..250
 /label= Mature_TNF-delta
 /note= "Tumour necrosis factor"
 76..83
 /label= Conserved domain I
 /note= "Region of high identity between TNF-delta
 and TNF-epsilon"
 113..121
 /label= Conserved domain II
 /note= "Region of high identity between TNF-delta
 and TNF-epsilon"
 129..138
 /label= Conserved domain III
 /note= "Region of high identity between TNF-delta
 and TNF-epsilon"

FT and TNF-epsilon"
 FT Domain 143..154
 /label= Conserved domain IV
 /note= "Region of high identity between TNF-delta
 and TNF-epsilon"
 FT Domain 155..171
 /note= "TNF family signature sequence"
 FT Domain 160..171
 /label= Conserved domain V
 /note= "Region of high identity between TNF-delta
 and TNF-epsilon"
 FT Domain 183..193
 /label= Conserved domain VI
 /note= "Region of high identity between TNF-delta
 and TNF-epsilon"
 FT Domain 196..201
 /label= Conserved domain VII
 /note= "Region of high identity between TNF-delta
 and TNF-epsilon"
 FT Domain 208..212
 /label= Conserved domain VIII
 /note= "Region of high identity between TNF-delta
 and TNF-epsilon"
 FT Domain 215..226
 /label= Conserved domain IX
 /note= "Region of high identity between TNF-delta
 and TNF-epsilon"
 FT Domain 229..236
 /label= Conserved domain X
 /note= "Region of high identity between TNF-delta
 and TNF-epsilon"
 FT Domain 246..250
 /label= Conserved domain XI
 /note= "Region of high identity between TNF-delta
 and TNF-epsilon"
 FT Domain
 FT WO200196528-A2.
 XX
 PD 20-DEC-2001.
 XX
 PF 14-JUN-2001; 2001WO-US19026.
 XX
 PR 15-JUN-2000; 2000US-211537P.
 PR 23-OCT-2000; 2000US-241952P.
 PR 13-DEC-2000; 2000US-254875P.
 PR 16-MAR-2001; 2001US-276248P.
 PR 23-MAR-2001; 2001US-277978P.
 PR 25-MAY-2001; 2001US-293499P.
 (HUMA-) HUMAN GENOME SCI INC.
 PI Yu G, Ni J, Gentz RL, Dillon PJ, Hilbert D;
 XX WPI; 2002-130727/17.
 DR N-PSDB; ABK13401.
 XX
 PT Novel multimeric human tumour necrosis factor delta or epsilon protein
 PT useful for treating cancer, immune system disorders, infection,
 PT cardiovascular disorders, liver disease, cardiomyopathy, diabetes and
 PT psoriasis
 XX
 PS Claim 1; Fig 6A-B; 344pp; English.
 XX
 CC The invention describes a multimeric human tumour necrosis factor (TNF)
 CC delta or epsilon protein (I). (I) or a composition containing them (II)
 CC are useful for modulating immunoglobulin production or proliferation of B
 CC cells. (I) or (II) is useful for treating a disease or disorder of the
 CC immune system, preferably an autoimmune disease (e.g. Sjogren's syndrome,
 CC systemic lupus erythematosus or common variable immunodeficiency (CVID));
 CC an immunodeficiency e.g. acquired immunodeficiency syndrome (AIDS);
 CC cancer of the immune system (e.g. Hodgkin's disease, non-Hodgkin's
 CC lymphoma, multiple myeloma and chronic lymphocytic leukaemia (CLL)); in
 CC the diagnosis and treatment or prevention of cancer, lymphoproliferative

CC disorder, bacterial and viral infections, osteoporosis, atherosclerosis,
 CC pain, cardiovascular disorders (e.g. stroke), allergy, inflammation,
 CC neurodegenerative disease (e.g. Alzheimer's disease), liver disease (e.g.
 CC cirrhosis), cardiomyopathy, diabetes, asthma, psoriasis, septic shock,
 CC glomerulonephritis, ulcerative colitis, arteriosclerosis; for promoting
 CC angiogenesis and wound healing; as a diagnostic research reagent; as an
 CC agent to target and kill cells expressing a TNFdelta and/or TNFepsilon
 CC receptor; in apoptosis of transformed cell lines; mediation of cell
 CC activation and proliferation; and as an immunogen to produce (II). (II)
 CC is useful to purify, detect and target (I), for measuring levels of (I)
 CC in biological samples, for immunophenotyping samples, and to treat,
 CC inhibit or prevent diseases and disorders associated with aberrant
 CC expression and/or activity of (I). This is the amino acid sequence of
 CC human tumour necrosis factor delta (TNF-delta) splicing variant #2,
 CC described in the method of the invention.
 XX
 SQ Sequence 250 AA;
 Query Match 73.2%; Score 183; DB 23; Length 250;
 Best Local Similarity 100.0%; Pred. No. 2.4e-169;
 Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 68 TGGPSQNGEGYPMQSLPEQSSDALBAMWNGERSRKRAVLTKOKKHSHVLHVPINATS 127
 DB 68 TGGPSQNGEGYPMQSLPEQSSDALBAMWNGERSRKRAVLTKOKKHSHVLHVPINATS 127
 QY 128 KDDSDVTEVMQDALRGRGLAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQVVSREGQ 187
 DB 128 KDDSDVTEVMQDALRGRGLAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQVVSREGQ 187
 QY 188 GROETLFRICRSMPSHPDRAYNSCYSAGVFHLHOGDILSVIIPARAKLNLSPHGTFLGF 247
 DB 188 GROETLFRICRSMPSHPDRAYNSCYSAGVFHLHOGDILSVIIPARAKLNLSPHGTFLGF 247
 QY 248 VKL 250
 DB 248 VKL 250
 RESULT 22
 AAY09551
 ID AAY09551 standard; Protein; 233 AA.
 XX
 AC AAY09551;
 XX
 DT 21-JUL-1999 (first entry)
 XX
 DE Human TRAILLK-3 protein.
 XX
 KW Human; TRAILLK-3; TNF ligand family; tumour necrosis factor; Apo-2L;
 KW cancerous growth; breast cancer; feed additive.
 OS Homo sapiens.
 XX
 PN EP919620-A2.
 XX
 PD 02-JUN-1999.
 XX
 PF 25-NOV-1998; 98EP-0309670.
 XX
 PR 11-AUG-1998; 98US-0096171.
 PR 26-NOV-1997; 97US-0066576.
 XX
 PA (ELIL) LILLY & CO ELI.
 XX
 PI 'Song HY;
 XX
 DR WPI; 1999-304824/26.
 DR N-PSDB; AAX56316.
 XX
 PT New Tumour Necrosis Factor Family Ligand, useful for treatment of
 PT cancer
 XX

PR 04-NOV-1998; 98US-0106976.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Leonardo MJ, Wang J, Jiang D;
XX
DR WPI; 2000-365575/31.
DR N-PSDB; AAA27732.
XX
PT Novel nucleic acids encoding tumor necrosis factor family polypeptides
PT termed as Death Receptor ligands useful for stimulating immune response
PT and inducing apoptosis comprising a specific nucleotide sequence
XX
PS Claim 6; Fig 1A; 80pp; English.
XX
CC The present sequence is that of human death receptor ligand 1
CC (DRL-1), a novel member of the tumour necrosis factor (TNF) family,
CC also termed TNF-gamma or TNF-like ligand (TLN). The sequence was
CC deduced from cDNA (see AAA27732) isolated from a lymphoma cell line.
CC DRL-1 is expressed as a 1.8 kb transcript in heart, placenta, lung,
CC kidney and pancreas. In the lymphoid tissue, it is expressed in
CC the peripheral lymphoid organs but not in the thymus or foetal
CC liver. The invention provides human and murine DRL polypeptides,
CC nucleic acids and antibodies. DRL-1 polypeptides are used in
CC claimed methods of stimulating an immune response and of inducing
CC apoptosis in a population of T-cells. Antibodies to DRL-1 are
CC used in claimed methods of suppressing an immune response,
CC inhibiting a T-cell response associated with transplant rejection
CC or graft versus host disease, inhibiting apoptosis in a population
CC of T cells, and of stimulating the membrane-bound form of DRL-1.
XX
SQ Sequence 250 AA;
Query Match 61.6%; Score 154; DB 21; Length 250;
Best Local Similarity 100.0%; Pred. No. 3.5e-141;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 97 GERSRKRRAVLTKQKKHSHLVLPINATSKDSDVTEVMQPALRRGRGLQAGYGV 156
DB 97 GERSRKRRAVLTKQKKHSHLVLPINATSKDSDVTEVMQPALRRGRGLQAGYGV 156
QY 157 IQDAGVYLLYSQVLFQDVTFTMGQVVSREGGQRETFLFRICRSMPSHPDRAYNSCYSAGV 216
DB 157 IQDAGVYLLYSQVLFQDVTFTMGQVVSREGGQRETFLFRICRSMPSHPDRAYNSCYSAGV 216
QY 217 FHLHOGDILSVIIPRAKATNLSPHGTFLGFVKL 250
DB 217 FHLHOGDILSVIIPRAKATNLSPHGTFLGFVKL 250
RESULT 25
AAE15502
ID AAE15502 standard; Protein; 250 AA.
XX
AC AAE15502;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human APRIL G70 protein #2.
XX
KW Human; transmembrane activator and intracellular CAML interactor; TACI;
KW cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KW rheumatoid arthritis; atherosclerosis; APRIL G70.
XX
OS Homo sapiens.
XX
XX WO200187979-A2.
XX

PD 22-NOV-2001.
XX
PF 14-MAY-2001; 2001WO-US15567.
XX
PR 12-MAY-2000; 2000US-204039P.
PR 27-JUN-2000; 2000US-214591P.
PR 14-MAY-2001; 2001US-0214591.
XX
PA (AMGE-) AMGEN INC.
XX
PI Theill LE, Yu G;
XX
DR WPI; 2002-06686/09.
XX
PT Inhibiting activity of B cell maturation protein and/or transmembrane
PT activator and intracellular cyclophilin ligand interactor, by
PT administering a binding partner for APRIL, a tumor necrosis factor
PT family ligand
XX
PS Disclosure; Fig 3; 94pp; English.
XX
CC The invention relates to a method for inhibiting TACI (transmembrane
CC activator and intracellular CAML interactor) and/or B cell maturation
CC protein (BCMA) activity in a mammal. The method comprises administering
CC a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
CC BCMA extracellular consensus sequence, but not the extracellular region
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC lymphoproliferative disorders, one or more solid tumours such as lung,
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
CC disease), drug and insect sting allergy, inflammatory bowel disease
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC with leucocyte infiltration of the skin or organs. The present sequence
XX
SQ Sequence 250 AA;
Query Match 61.6%; Score 154; DB 23; Length 250;
Best Local Similarity 100.0%; Pred. No. 3.5e-141;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 97 GERSRKRRAVLTKQKKHSHLVLPINATSKDSDVTEVMQPALRRGRGLQAGYGV 156
DB 97 GERSRKRRAVLTKQKKHSHLVLPINATSKDSDVTEVMQPALRRGRGLQAGYGV 156
QY 157 IQDAGVYLLYSQVLFQDVTFTMGQVVSREGGQRETFLFRICRSMPSHPDRAYNSCYSAGV 216
DB 157 IQDAGVYLLYSQVLFQDVTFTMGQVVSREGGQRETFLFRICRSMPSHPDRAYNSCYSAGV 216
QY 217 FHLHOGDILSVIIPRAKATNLSPHGTFLGFVKL 250
DB 217 FHLHOGDILSVIIPRAKATNLSPHGTFLGFVKL 250
RESULT 26
AAV60542
ID AAV60542 standard; Protein; 260 AA.
XX
AC AAV60542;
XX
DT 31-JAN-2000 (first entry)
XX
DE Human normal bladder tissue EST encoded protein 214.
XX
KW Human; bladder; treatment; EST; expressed sequence tag; cytostatic;
KW cancer; gene therapy.
XX

OS Homo sapiens.
XX
PN DE19818620-A1.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1998; 98DE-1018620.
XX
PR 21-APR-1998; 98DE-1018620.
XX
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
XX
PI Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;
XX
DR WPI; 1999-602416/52.
DR N-PSDB; AA242229.
XX
PT New polypeptides and their nucleic acids, useful for treatment of
PT bladder tumour and identification of therapeutic agents -
XX
XX Claim 23; Page 331; 366pp; German.
XX
CC This invention describes novel polypeptide fragment sequences (I) and
CC their encoding nucleic acids (II) which are highly expressed in normal
CC bladder tissue and have cytostatic activity. (II) are used for
CC recombinant expression of (I) and to isolate complete genes. (I) are
CC used to identify agents suitable for the treatment of bladder tumours,
CC to directly treat this form of cancer (including expression from gene
CC therapy vectors), or are used in a preparation for cancer treatment. (I)
CC is also used for the generation of specific antibodies. (II) are
CC identified by assembling ESTs (expressed sequence tags) from a
CC particular tissue type before comparison of expression patterns. This
CC allows a significantly longer fragment of the gene to be revealed, and
CC therefore reduces the number of failures because of ESTs from different
CC libraries representing different parts of the same unknown gene
CC disorienting the estimated frequency of occurrence in a particular tissue.
CC AAY60329-Y60591 represent protein fragments encoded by the human normal
CC bladder tissue cDNA library derived EST fragments represented in
CC AA242122-Z42248.
XX
SQ Sequence 260 AA;
XX
Query Match 61.6%; Score 154; DB 20; Length 260;
Best Local Similarity 100.0%; Pred. No. 3.6e-141; Indels 0; Gaps 0;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 97 GERSRKRRAVLTKQKKQHSVLHLPINATSKDSDVTEVMQPALRRGRGLQAQGYGVR 156
107 GERSRKRRAVLTKQKKQHSVLHLPINATSKDSDVTEVMQPALRRGRGLQAQGYGVR 166
QY 157 IQDAGVYLLYSQVLFQDVTFTMGQVVSREGGRQETLFRICIRSMPSHPDRAYNSCYSAGV 216
167 IQDAGVYLLYSQVLFQDVTFTMGQVVSREGGRQETLFRICIRSMPSHPDRAYNSCYSAGV 226
QY 217 FHLHQGDILSVIIPRARAKLNLSPHGTFLGFVKL 250
227 FHLHQGDILSVIIPRARAKLNLSPHGTFLGFVKL 260
Db
RESULT 27
AAB54342
ID AAB54342 standard; Protein; 260 AA.
XX
AC AAB54342;
XX
DT 09-MAR-2001 (first entry)
XX
DE Human pancreatic cancer antigen protein sequence SEQ ID NO:794.
XX
KW .Human; pancreas; pancreatic cancer; pancreatic cancer antigen;
KW detection; diagnosis; identification; cytostatic; neuroprotective;
KW nootropic; immunomodulatory; relaxant; contraceptive; gynaecological;
KW antiinflammatory; cardiant; gene therapy; chromosome mapping;

KW linkage analysis; tissue identification; tissue typing; forensic;
KW neutral; immune system; muscular; reproductive; gastrointestinal;
KW pulmonary; cardiovascular; renal; proliferative.
XX
OS Homo sapiens.
XX
PN WO200055320-A1.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US05989.
XX
PR 12-MAR-1999; 99US-0124270.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2000-579444/54.
DR N-PSDB; AAC99107.
XX
PT New nucleic acid that is a pancreatic cancer antigen for preventing,
PT treating, or ameliorating a medical condition, particular pancreatic
PT cancer, or for use in assays for diagnosing a pathological condition -
XX
XX Claim 11; Page 1235-1236; 1379pp; English.
XX
CC AAC98773 to AAC99231 encode the human pancreatic cancer associated
CC proteins, called pancreatic cancer antigens, given in AAB54008 to
CC AAB54466. The human pancreatic cancer antigens have cytostatic,
CC neuroprotective, nootropic, immunomodulatory, relaxant, contraceptive,
CC gynaecological, cardiant and antiinflammatory activities, and can be used
CC in gene therapy. The polynucleotide and proteins can be used for
CC preventing, treating, or ameliorating a medical condition or in assays
CC for diagnosing a pathological condition or a susceptibility to one in a
CC subject. Binding partners to the proteins and the activity of the
CC proteins can be identified. The pancreatic cancer antigens can be used to
CC detect, treat or prevent pancreatic disorders, especially cancer.
CC Agonists and antagonists to the antigens can be screened for. The
CC pancreatic cancer antigen polynucleotides can be used to design nucleic
CC acid hybridisation probes that can be used in chromosome mapping, linkage
CC analysis, tissue identification and/or typing and a variety of forensic
CC and diagnostic methods. The proteins can be used to generate antibodies
CC which are used to purify, detect and target the polypeptides, including
CC both in vivo and in vitro diagnostic and therapeutic methods. The
CC proteins can be used to treat or prevent neural, immune system, muscular,
CC reproductive, gastrointestinal, pulmonary, cardiovascular, renal or
CC proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent
CC sequences used in the exemplification of the present invention.
XX
SQ Sequence 260 AA;
XX
Query Match 61.6%; Score 154; DB 21; Length 260;
Best Local Similarity 100.0%; Pred. No. 3.6e-141; Indels 0; Gaps 0;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 97 GERSRKRRAVLTKQKKQHSVLHLPINATSKDSDVTEVMQPALRRGRGLQAQGYGVR 156
107 GERSRKRRAVLTKQKKQHSVLHLPINATSKDSDVTEVMQPALRRGRGLQAQGYGVR 166
QY 157 IQDAGVYLLYSQVLFQDVTFTMGQVVSREGGRQETLFRICIRSMPSHPDRAYNSCYSAGV 216
167 IQDAGVYLLYSQVLFQDVTFTMGQVVSREGGRQETLFRICIRSMPSHPDRAYNSCYSAGV 226
QY 217 FHLHQGDILSVIIPRARAKLNLSPHGTFLGFVKL 250
227 FHLHQGDILSVIIPRARAKLNLSPHGTFLGFVKL 260
Db
RESULT 28
AAE15482
ID AAE15482 standard; Protein; 248 AA.
XX

AC AAE15402;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human APRIL G70 protein #1.
XX
KW Human; transmembrane activator and intracellular CAML interactor; TACI;
KW cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KW rheumatoid arthritis; atherosclerosis; APRIL G70.
XX
OS Homo sapiens.
XX
PN WO200187979-A2.
XX
XX 22-NOV-2001.
XX
XX 14-MAY-2001; 2001WO-US15567.
XX
PR 12-MAY-2000; 2000US-204039P.
PR 27-JUN-2000; 2000US-214591P.
PR 14-MAY-2001; 2001US-0214591.
XX
PA (AMGE-) AMGEN INC.
XX
PI Theill LE, Yu G;
XX
DR WPI; 2002-066686/09.
DR N-PSDB; AAD24708.
XX
XX
PT Inhibiting activity of B cell maturation protein and/or transmembrane
PT activator and intracellular cyclophilin ligand interactor, by
PT administering a binding partner for APRIL, a tumor necrosis factor
PT family ligand -
XX
PS Disclosure; Fig 1; 94pp; English.
XX
XX The invention relates to a method for inhibiting TACI (transmembrane
CC activator and intracellular CAML interactor) and/or B cell maturation
CC protein (BCMA) activity in a mammal. The method comprises administering
CC a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
CC BCMA extracellular consensus sequence, but not the extracellular region
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC lymphoproliferative disorders, one or more solid tumours such as lung,
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
CC disease), drug and insect sting allergy, inflammatory bowel disease
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC with leucocyte infiltration of the skin or organs. The present sequence
CC is human APRIL G70 protein.
XX
SQ Sequence 248 AA;
Query Match 60.8%; Score 152; DB 23; Length 248;
Best Local Similarity 100.0%; Pred. No. 3e-139;
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 157 IQDAGVYLLYSQVLFQDVTFTMGQVVSREGGROETLFR CIRSMPSHPDRAYNSCYSAGV 216
QY 217 FHLHQGDILSVIIPRARA KLNSPHGTF LGFV 248
Db 217 FHLHQGDILSVIIPRARA KLNSPHGTF LGFV 248
RESULT 29
AAW88369
ID AAW88369 standard; Protein; 147 AA.
XX
AC AAW88369;
XX
DT 26-APR-1999 (first entry)
XX
DE Tumour necrosis factor-gamma soluble polypeptide.
XX
KW Tumour necrosis factor-gamma; TNF-gamma; human; inflammation;
KW cancer; tumour; metastasis; graft versus host disease;
KW drug screening; therapy; diagnosis.
XX
OS Homo sapiens.
XX
PN WO9900518-A1.
XX
PD 07-JAN-1999.
XX
PF 12-JUN-1998; 98WO-US12101.
XX
PR 26-JUN-1997; 97US-0883086.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Wiley SR;
XX
DR WPI; 1999-095761/08.
XX
XX Tumour necrosis factor gamma detects target polynucleotides - useful
PT for, e.g. treating inflammation, cancer and graft versus host
PT disease
XX
XX Claim 16; Page 85; 106pp; English.
XX
PS This soluble polypeptide comprises amino acid residues 104-250 of
XX human tumour necrosis factor gamma (TNFG, see AAW88368), a novel
CC member of the TNF family of ligands. The soluble polypeptide
CC interacts with the cognate receptor, and induces biological
CC activity. It can be prepared by recombinant DNA methods, and used
CC to treat deficiencies of TNFG and disease conditions ameliorated by
CC TNFG. Antibodies, antagonists and inhibitors of the polypeptide
CC may be used to treat TNFG-associated diseases, tumours or
CC metastases, and to screen for, diagnose and monitor conditions
CC attributable to TNFG, especially inflammation, cancer and graft
CC versus host disease.
XX
SQ Sequence 147 AA;
Query Match 58.8%; Score 147; DB 20; Length 147;
Best Local Similarity 100.0%; Pred. No. 1.4e-134;
Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 GERSRKRRAVLTKOKKQSHV LHPINATSKDSDVTEVMQPALRRGRGLQAQGYGVR 156
Db 97 GERSRKRRAVLTKOKKQSHV LHPINATSKDSDVTEVMQPALRRGRGLQAQGYGVR 156
QY 157 IQDAGVYLLYSQVLFQDVTFTMGQVVSREGGROETLFR CIRSMPSHPDRAYNSCYSAGV 216

QY 104 RAVLTOKOKKQSHV LHPINATSKDSDVTEVMQPALRRGRGLQAQGYGVR IQDAGVY 163
Db 1 RAVLTOKOKKQSHV LHPINATSKDSDVTEVMQPALRRGRGLQAQGYGVR IQDAGVY 60
QY 164 LLYSQVLFQDVTFTMGQVVSREGGROETLFR CIRSMPSHPDRAYNSCYSAGV FHLHQGD 223
Db 61 LLYSQVLFQDVTFTMGQVVSREGGROETLFR CIRSMPSHPDRAYNSCYSAGV FHLHQGD 120
QY 224 ILSV IIPRARA KLNSPHGTF LGFVKL 250
Db 121 ILSV IIPRARA KLNSPHGTF LGFVKL 147

RESULT	30
AAO14134	
ID	AAO14134 standard; Protein; 177 AA.
XX	
XX	
AC	AAO14134;
XX	
DT	02-MAY-2002 (first entry)
XX	
DE	Protein of a FLAG tagged human APRIL (soluble).
XX	
KW	Human transmembrane activator CAML interactor protein; TACI; cytostatic;
KW	cell proliferation; tumour; vulnerrary; renal cell cancer; mastocytoma;
KW	Kaposi's sarcoma; breast; ovarian carcinoma; rectal; throat; melanoma;
KW	colon; bladder; mammary adenocarcinoma; gastrointestinal; hyperplasia;
KW	pharyngeal squamous cell; stomach; cellular hyperproliferation; pannus;
KW	scleroderma; rheumatoid arthritis; scarring; mean survival time; liver;
KW	lung fibrosis; uterine; a proliferation inducing ligand.
XX	
OS	Homo sapiens.
XX	
XX	Synthetic.

FT	Key	Location/Qualifiers
FT	Peptide	1..15
FT		/note= "HA signal sequence tag"
FT	Region	16..23
FT		/note= "FLAG epitope tag"
FT	Region	24..31
FT		/note= "Short linker sequence"
FT	Region	32..177
FT		/note= "Soluble human APRIL sequence"

PN	WO200181417-A2.
XX	
PD	01-NOV-2001.
XX	
PF	27-APR-2001; 2001WO-US40626
XX	
PR	27-APR-2000; 2000US-199946P

PA (BIOJ) BIOGEN INC.
PA (APOT-) APOTTECH R & D SA.

PI Ambrose C, Thompson J, Schneider P, Rennert P;

DR WPI; 2002-062027/08.
DR N-PSDB; AAK98730.

Treating mammal for condition associated with undesired cell proliferation e.g., solid tumour or reducing solid tumour size located in mammal comprises administering transmembrane activator CAML interactor protein reagent -

PS Examples; Fig 9; 42pp; English..

This sequence represents the protein of a FLAG tagged human APRIL (A Proliferation Inducing Ligand) (soluble). The invention relates to treating a mammal for a condition associated with undesired cell proliferation (e.g. a solid tumour, or reducing the size of a solid tumour located on or in a mammal) comprising administering a transmembrane activator CAML interactor protein (TACI) reagent. The TACI reagent has cytostatic and vulnerary activity. Treating a mammal (e.g. human, cow, horse, dog, mouse, rat or cat) for a condition associated with undesired cell proliferation (e.g. cancer such as renal cell cancer, Kaposi's sarcoma, breast cancer, sarcoma, ovarian carcinoma, rectal cancer, throat cancer, melanoma, colon cancer, bladder cancer, mastocytoma, lung cancer, mammary adenocarcinoma, pharyngeal squamous cell carcinoma, gastrointestinal cancer or stomach cancer). The method is also useful for treating cellular hyperproliferation (hyperplasia) such as scleroderma, pannus formation in rheumatoid arthritis, post-surgical scarring and lung, liver and uterine fibrosis. The TACI reagent of the invention can extend mean survival time of a mammal by 25% as compared to the mean survival time of a mammal in the absence of administering the

CC TACI reagent. The TACI reagent also reduces the size of the tumour by 25%
CC or more.
XX
SQ Sequence 177 AA;

```

Query Match          58.4%; Score 146; DB 23; Length 177;
Best Local Similarity 100.0%; Pred. No. 1.5e-133;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 105 AVLTKQKQSHLVLPINATSKDDSDVTEVMQPALRRGGLQAQGYVRIQDAGVYL 164

Db 32 AVLTQKQKQHSVLHLPINATSKDDSDVTEVMWQPALRRGRLQAQGYGVRIQDAGVYL 91

QY 165 LYSQVLFDVTFMGOVSREGGRQETLFRCIRSMPSHPDRAVNSCYSAGVFHLHQGD 224

Db 92 LYSQVLFDVTFTMGQVSRREGQGRQETLFR CIRSMPSHPDRA YNSCY SAGVFHLHQGDI 151

QY 225 LSVIIPRAKLNLSPHGTF LGFVKL 250

db 152 LSVIIPRAKLNLSPHGTELGFKL 177

RESULT 31

AAE00505 standard; Protein; 172 AA.

AAE00505;

```
... 31-JUL-2001 (first entry)
DT
```

DE FLAG-human A Proliferation Inducing Ligand (APRIL) protein construct.

KW Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;

KW carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension

KW B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;

KW tumour necrosis factor; B cell maturation protein; BCMA; FLAG epitope

OS Homo sapiens

Synthetic.

FH	Key	Location/Qualifiers
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
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FT	/label= signal_peptide
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99	1
100	1

```
FT /label= Mature_FLAG-human_A_Proliferation_Inducing_Ligand
```

FT	Region	16..23
		-

XX

XX

XX

XX

PR 11-FEB-2000; 2000US-0181807.

XX

PA (APOT-) APOTECH R & D SA.

PI Schneider P, Thompson J, Cachero T, Ambrose C, Rennert P;

DR WPI; 2001-266242/27.

XX

PT proliferation such as cancer or carcinoma, comprises administering a

PT composition comprising A Proliferation Inducing Ligand Receptor

PT (APRIL-R) antagonist -
XX
PS Example 2; Fig 2; 85bp; English.
XX
CC The invention relates to a method of treating a mammal for a condition
CC associated with undesired cell proliferation such as cancer or
CC carcinoma. The method involves administering a composition comprising
CC A Proliferation Inducing Ligand Receptor (APRIL-R) also referred as
CC B cell maturation protein (BCM or BCMA) antagonist that antagonises the
CC interaction between APRIL and its cognate receptor(s). This method is
CC useful for treating undesired cell proliferation such as cancer or
CC carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,
CC prostate carcinoma, and other carcinomas whose proliferation is modulated
CC by APRIL. It is also useful for treating autoimmune diseases (Grave's
CC disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular
CC diseases, renal disorders, B-cell lympho-proliferative disorders,
CC immunosuppressive diseases, organ transplantation, inflammation and
CC human immunodeficiency virus (HIV), and for treating, suppressing or
CC altering an immune response involving a signalling pathway between
CC APRIL-R and its ligand. APRIL-R DNA is also useful in gene therapy.
CC The present sequence is FLAG-human A Proliferation Inducing Ligand
CC (APRIL) protein construct. This sequence comprises FLAG epitope,
CC followed by human APRIL extracellular domain. APRIL is a member of
CC Tumour Necrosis Factor (TNF) family of proteins.
XX
SQ Sequence 172 AA;

Query Match 56.8%; Score 142; DB 22; Length 172;
Best Local Similarity 100.0%; Pred. No. 1.1e-129;
Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 QKQKKQHSVLHLVPINATSKDSDVTEVMQPALRGRGLQAGYGVRIQDAGVYLLYSQ 168
DB 31 QKQKKQHSVLHLVPINATSKDSDVTEVMQPALRGRGLQAGYGVRIQDAGVYLLYSQ 90

QY 169 VLFQDVTFTMGQVVSREGQGRQETLFR CIRSMPSHPDRAYNSCYSAGVFHLHOGDILSVI 228
DB 91 VLFQDVTFTMGQVVSREGQGRQETLFR CIRSMPSHPDRAYNSCYSAGVFHLHOGDILSVI 150

QY 229 IPRARAKLNLSPHGTFLGFVKL 250
DB 151 IPRARAKLNLSPHGTFLGFVKL 172

RESULT 32
AAW37002
ID AAW37002 standard; Protein; 233 AA.
AAW37002;

DT 14-APR-1998 (first entry)
XX
DE Human tumour necrosis factor delta.
XX
KW Human; tumour necrosis factor delta; TNF-delta; TNF-epsilon; cancer;
KW tumour necrosis factor epsilon; T cell proliferation;
KW immune regulation; inflammatory response.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 231..233
FT /note= "Not given in the specification but present
FT if the cDNA is fully decoded"
XX
XX WO9733902-A1.
XX
XX 18-SEP-1997.
XX
XX 14-MAR-1996; 96WO-US03774.
XX
XX 14-MAR-1996; 96WO-US03774.
XX

PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Gentz RL, Ni J, Yu G;
XX
DR WPI; 1997-470810/43.
DR N-PSDB; AAV00493.
XX
PT Nucleic acid encoding human tumour necrosis factors delta and
PT epsilon - useful for destroying cancer cells, or mediating T cell
PT proliferation, immune regulation and inflammatory responses etc.
XX
PS Claim 18; Fig 1; 83bp; English.
XX
CC The present sequence represents human tumour necrosis factor (TNF)
CC delta. The TNF can be used to treat patients deficient in this factor
CC (optionally by in vivo expression). It is a ligand for TNF and can
CC destroy (by inducing apoptosis) some transformed cell lines (for tumour
CC treatment); mediate cell activity and proliferation (including T cells
CC to stimulate an immune response to viral, bacterial or parasitic
CC infections, also to eliminate autoreactive T cells in e.g. type I
CC diabetes), and is functionally linked as a primary mediator of immune
CC regulation and the inflammatory response. A typical application of the
CC protein, its agonists or antagonists is prevention of septic shock,
CC inflammation, cerebral malaria, human immunodeficiency virus activation,
CC graft-host reaction, bone resorption (osteoporosis), rheumatoid
CC arthritis and cachexia, also to promote wound healing (by upregulating
CC cell adhesion) and to regulate haematopoiesis. The protein can also be
CC used to isolate its cognate receptors (or receptor-encoding genes).
CC The cDNA can be used to produce recombinant proteins, and fragments of
CC it to isolate full-length or related sequences, for diagnostic detection
CC of mutations (indicative of disease or susceptibility) and for
CC chromosome identification. Analysis of patient samples for presence of
CC the new protein (e.g. using specific antibodies) can be used
CC diagnostically.
XX
SQ Sequence 233 AA;

Query Match 56.8%; Score 142; DB 18; Length 233;
Best Local Similarity 100.0%; Pred. No. 1.5e-129;
Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 QKQKKQHSVLHLVPINATSKDSDVTEVMQPALRGRGLQAGYGVRIQDAGVYLLYSQ 168
DB 92 QKQKKQHSVLHLVPINATSKDSDVTEVMQPALRGRGLQAGYGVRIQDAGVYLLYSQ 151

QY 169 VLFQDVTFTMGQVVSREGQGRQETLFR CIRSMPSHPDRAYNSCYSAGVFHLHOGDILSVI 228
DB 152 VLFQDVTFTMGQVVSREGQGRQETLFR CIRSMPSHPDRAYNSCYSAGVFHLHOGDILSVI 211

QY 229 IPRARAKLNLSPHGTFLGFVKL 250
DB 212 IPRARAKLNLSPHGTFLGFVKL 233

RESULT 33
AAB08661
ID AAB08661 standard; Protein; 136 AA.
AAB08661;
XX
AC AAB08661;
XX
DT 02-JAN-2001 (first entry)
XX
DE A fragment of human neutrokin-alpha polypeptide.
XX
KW Human; neutrokin-alpha; tumor; tumor metastasis; infection;
KW immunodeficiency; inflammatory disease; lymphadenopathy; dermatitis;
KW autoimmune disease; graft versus host disease; immune regulation;
KW severe combined immunodeficiency-X-linked agammaglobulinemia;
KW kappa chain deficiency; B cell lymphoproliferative disorder; purpura;
KW Wiskott-Aldrich syndrome; systemic lupus erythematosus; myocarditis;
KW idiopathic thrombocytopenia purpura; hemolytic anemia; neuritis;
KW allergic encephalomyelitis; relapsing polychondritis; glomerulonephritis;
KW rheumatic heart disease; multiple sclerosis; uveitis ophthalmia;
KW

```

KW polyendocrinopathy; Reiter's disease; autoimmune pulmonary inflammation;
KM myeloprotection; stem cell mobilization; leukemia.
XX
OS Homo sapiens.
PN WO200050597-A2.
XX
PD 31-AUG-2000.
XX
PF 22-FEB-2000; 2000WO-US04336.
XX
PR 23-FEB-1999; 99US-0255794.
PR 02-MAR-1999; 99US-0122388.
PR 12-MAR-1999; 99US-0124097.
PR 26-MAR-1999; 99US-0126599.
PR 02-APR-1999; 99US-0127598.
PR 16-APR-1999; 99US-0130412.
PR 23-APR-1999; 99US-0130696.
PR 27-APR-1999; 99US-0131278.
PR 29-APR-1999; 99US-0131673.
PR 28-MAY-1999; 99US-0136784.
PR 06-JUL-1999; 99US-0142659.
PR 27-JUL-1999; 99US-0145824.
PR 24-NOV-1999; 99US-0167239.
PR 03-DEC-1999; 99US-0168624.
PR 16-DEC-1999; 99US-0171108.
PR 23-DEC-1999; 99US-0171626.
PR 14-JAN-2000; 2000US-0176015.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ni J, Ebner R, Yu G;
XX
DR WPI; 2000-572093/53.
XX
PT Novel cytokine neutrokin-alpha, its splicing variant, neutrokin-alpha
PT SV polypeptides useful for treating tumor, tumor metastasis, microbial
PT infections, immunodeficiency, inflammatory diseases, lymphadenopathy
PT
XX
PS Disclosure; Page 107-108; 414pp; English.
XX
CC The present sequence represents a fragment of human neutrokin-alpha
CC polypeptide. Neutrokin-alpha polypeptides are used to treat, prevent,
CC prognosis and diagnose tumor and tumor metastasis, infections by bacteria,
CC viruses and other parasites, immunodeficiencies, inflammatory diseases,
CC lymphadenopathy, autoimmune diseases, graft versus host disease, to
CC mediate immune regulation and inflammatory responses. Diseases which may
CC be treated include severe combined immunodeficiency (SCID)-X-linked
CC agammaglobulinemia, kappa chain deficiency, B cell lymphoproliferative
CC disorder (BLPD), Wiskott-Aldrich syndrome, systemic lupus erythematosus,
CC idiopathic thrombocytopenia purpura, hemolytic anemia, dermatitis,
CC allergic encephalomyelitis, myocarditis, relapsing polychondritis,
CC rheumatic heart disease, glomerulonephritis, multiple sclerosis,
CC Neuritis, Uveitis Ophthalmia, Polyendocrinopathies, Purpura
CC (e.g. Henloch-Schoenlein purpura), Reiter's Disease, and Autoimmune
CC Pulmonary Inflammation. Neutrokin-alpha is useful for immune enhancement
CC or suppression, myeloprotection, stem cell mobilization, acute and
CC chronic inflammatory control and treatment of leukemia.
XX
SQ Sequence 136 AA;

```

```

Query Match 54.4%; Score 136; DB 21; Length 136;
Best Local Similarity 100.0%; Pred. No. 6.2e-124;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 115 HSQLHLVPINATSKDSDVTEVMQPALRRGRLQAQGYGVRIQDAGVYLLYSQVLFQDV 174
Db 1 HSQLHLVPINATSKDSDVTEVMQPALRRGRLQAQGYGVRIQDAGVYLLYSQVLFQDV 60
QY 175 TFTMGQVNSREGQROETLFCIRSMPSHPRAVNSCYSAVFHLHOGDILSVIPRARA 234
Db 61 TFTMGQVNSREGQROETLFCIRSMPSHPRAVNSCYSAVFHLHOGDILSVIPRARA 120

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```

QY 235 KLNLSPHGTFGLGFVKL 250
Db 121 KLNLSPHGTFGLGFVKL 136

```

RESULT 34

AAU79142

AAU79142 standard; Protein; 136 AA.

AAU79142;

02-JUL-2002 (first entry)

Human APRIL (a proliferation-inducing ligand) protein #1.

Human; Neutrokin-alpha; antibody; immunogen; B-cell cancer;

autoimmune disease; Sjogre's syndrome; systemic lupus erythematosus;

rheumatoid arthritis; chronic lymphocytic leukemia; multiple myeloma;

Hodgkin's lymphoma; non-Hodgkin's lymphoma; hypergammaglobulinemia;

APRIL; a proliferation-inducing ligand.

Homo sapiens.

Key	Location/Qualifiers
Region	1..8
Region	/label= Beta_sheet_A
Region	28..29
Region	/label= Beta_sheet_A'
Region	33..35
Region	/label= Beta_sheet_B'
Region	39..41
Region	/label= Beta_sheet_B
Region	47..60
Region	/label= Beta_sheet_C
Region	66..71
Region	/label= Beta_sheet_D
Region	76..87
Region	/label= Beta_sheet_E
Region	94..103
Region	/label= Beta_sheet_F
Region	108..115
Region	/label= Beta_sheet_G
Region	128..136
Region	/label= Beta_sheet_H

WO200218620-A2.

07-MAR-2002.

15-AUG-2001; 2001WO-US25549.

15-AUG-2000; 2000US-225628P.

23-AUG-2000; 2000US-227008P.

22-SEP-2000; 2000US-234338P.

17-OCT-2000; 2000US-240806P.

30-NOV-2000; 2000US-250020P.

06-MAR-2001; 2001US-276248P.

25-MAY-2001; 2001US-293499P.

07-JUN-2001; 2001US-296122P.

13-JUL-2001; 2001US-304809P.

(HUMA-) HUMAN GENOME SCI INC.

Yu G, Ebner R, Ni J, Rosen CA, Ullrich S;

WPI; 2002-304259/34.

An isolated antibody or portion that specifically binds to a protein useful in the treatment of diseases such as hypergammaglobulinemia and cancer -

Example 6; Fig 7; 482pp; English.

XX		The present invention relates to a new antibody, or portion, that
CC		specifically binds to a protein which has a 285 or 250 amino acid
CC		sequence as fully defined in the specification. The antibody of the
CC		invention is useful in treating a disease or disorder such as cancer,
CC		especially B-cell cancer, autoimmune diseases such as Sjogren's
CC		Syndromic, systemic lupus erythematosus, rheumatoid arthritis, chronic
CC		lymphocytic leukaemia, multiple myeloma, Hodgkin's lymphoma,
CC		non-Hodgkin's lymphoma or hypergammaglobulinemia, or in diagnosing a
CC		disease or disorder comprising assaying expression of Neutrokin-alpha
CC		and APRIL (a proliferation-inducing ligand) in cells or body fluids using
CC		antibodies and comparing the Neutrokin-alpha and APRIL expression level
CC		with a standard Neutrokin-alpha and APRIL expression level, whereby an
CC		increase or decrease in the assayed Neutrokin-alpha and APRIL expression
CC		level compared to the standard levels is indicative of a disease or
CC		disorder. The present amino acid sequence represents the human APRIL
CC		protein #1 of the invention.
XX		
SO	Sequence	136 AA;
	Query Match	54.4%; Score 136; DB 23; Length 136;
	Best Local Similarity	100.0%; Pred. No. 6.2e-124;
	Matches 136; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Oy	115 HSVLHLPINATSKDSDVTEVMQPALRRGRGLQAQGYGVRIODAGVYLLYSQVLFQDV	174
Dd	1 HSVLHLVPINATSKDSDVTEVMQPALRRGRGLQAQGYGVRIODAGVYLLYSQVLFQDV	60
Oy	175 TFTMGQVSREGQGRETFLRCIRSMESHDPDRAYNSCYSAGVFHLLHGGDILSVIIPRARA	234
Dd	61 TFTMGQVSREGQGRETFLRCIRSMESHDPDRAYNSCYSAGVFHLLHGGDILSVIIPRARA	120
Oy	235 KLNLSPHGTFLGFKVL	250
Dd	121 KLNLSPHGTFLGFKVL	136
	RESULT 35	
ID	AAE07877	standard; Protein; 248 AA.
AC	AAE07877;	
DT	01-NOV-2001	(first entry)
DE		Human APRIL protein.
XX		
KW		Human; tumour necrosis factor; TNF; APBF; APRIL; BAFF; therapy; melanoma;
KW		immune system-related disorder; cancer; renal cell; breast; stomach;
KW		rectal; colon; throat; bladder; ovarian carcinoma; cellular disorder;
KW		gastrointestinal; scleroderma; Kaposi's sarcoma; chronic leukaemia;
KW		squamous cell carcinoma; hyperproliferative condition; pannus formation;
KW		rheumatoid arthritis; postsurgical scarring; fibrosis; liver; uterine;
KW		lung; immunodeficiency; inflammatory disease; lymphadenopathy; vulnerary;
KW		autoimmune disease; graft versus host disease; dermatological;
KW		antiinflammatory; immunosuppressive; cytostatic.
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Misc-difference 16	/note= "Encoded by GGC"
FT	Region	29..48
FT	Misc-difference 32..33	/label= Transmembrane_region
FT	Misc-difference 43	/note= "Encoded by TGTTTGTACT"
FT	Misc-difference 70..72	/note= "Encoded by TGT"
FT	Misc-difference 102..104	/note= "Encoded by CCTCCCAG"
FT	Misc-difference 108..117	/note= "Encoded by AGGAGACA"
FT	Region	108..117

FT	/note= "N-terminal of the recombinant soluble APRIL	
FT	sequence"	
FT	Modified-site	123
FT	/note= "N-glycosylated"	
FT	Misc-difference	174
FT	/note= "Encoded by ACT"	
FT	Misc-difference	176
FT	/note= "Encoded by ACC"	
FT	Misc-difference	220..221
FT	/note= "Encoded by CAAGCGAT"	
XX		
PN	WO200158949-A2.	
XX		
PD	16-AUG-2001.	
XX		
PF	08-FEB-2001; 2001WO-US04121.	
XX		
PR	11-FEB-2000; 2000US-0181670.	
XX		
PA	(BIOJ) BIOGEN INC.	
XX		
PI	Rennert PD, Thompson JS, Ambrose C, Cachero TG;	
XX		
DR	WPI; 2001-514644/56.	
DR	N-PSDB; MAD14415.	
PT	New heteromeric ligand of tumor necrosis factor (TNF) family, useful	
PT	for diagnosis, treatment of immune system-related disorders in humans,	
PT	comprises TNF-family member APRIL subunit linked non-covalently to	
PT	TNF-family member BAF subunit	
XX		
PS	Claim 2; Fig 1a; 42pp; English.	
XX		
CC	The present invention relates to an isolated heteromeric ligand of	
CC	tumour necrosis factor (TNF)-family, referred to as APBF comprising a	
CC	TNF-family member APRIL subunit linked non-covalently to TNF-family	
CC	member BAF subunit. APBF is useful for diagnosis or treatment of	
CC	various immune system-related disorders in mammals, preferably humans.	
CC	Such disorders include cancer, including cellular disorders, for e.g.	
CC	renal cell cancer, Kaposi's sarcoma, chronic leukaemia, breast cancer,	
CC	sarcoma, ovarian carcinoma, rectal cancer, throat cancer, melanoma,	
CC	colon cancer, bladder cancer, squamous cell carcinoma and	
CC	gastrointestinal or stomach cancer, cellular hyperproliferative	
CC	conditions, such as scleroderma, pannus formation in rheumatoid	
CC	arthritis, postsurgical scarring and lung, liver and uterine fibrosis	
CC	and immunodeficiencies, inflammatory diseases, lymphadenopathy,	
CC	autoimmune diseases and graft versus host disease. APBF is also useful	
CC	for producing monoclonal or polyclonal antibodies and for identifying	
CC	novel modulators affecting biological function and receptors interacting	
CC	with APBF. The present sequence is human APRIL protein.	
XX		
SO	Sequence 248 AA;	
QY	Query Match	52.0%; Score 130; DB 22; Length 248;
QY	Best Local Similarity	100.0%; Pred. No. 7.1e-118;
QY	Matches 130; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Db	44	AMALLTQOTELQSLRREVSRLOGTGCPSPQNGEGYFWQSLPEQSSDALLEAWENGERSRKRR 104
QY	105	AVLTQOKQKHSHLVPINATSKDDSDVTEVMQPALRRGRGLQAGYGVRIQDAGVYL 164
Db	104	AVLTQOKQKHSHLVPINATSKDDSDVTEVMQPALRRGRGLQAGYGVRIQDAGVYL 163
QY	165	LYSQVLFQDV 174
Db	164	LYSQVLFQDV 173

XX AAB64873;
AC
XX
DT 23-MAR-2001 (first entry)
XX
DE Gene 44 human secreted protein homologous amino acid sequence #159.
XX
KW Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic;
KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
KW nootropic; neuroprotective; antibacterial; virucide; fungicide;
KW ophthalmological; autoimmune disease; hyperproliferative disorder;
KW cardiovascular disorder; cerebrovascular disorder; infection; chemotaxis;
KW nervous system disorder; ocular disorder; skin aging; wound healing;
KW food additive; tissue regeneration.
XX
OS Homo sapiens.
XX
PN WO200077256-A1.
XX
PF 01-JUN-2000; 2000WO-US14963.
XX
PR 11-JUN-1999; 99US-0138631.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Komatsoulis GA;
XX
DR WPI, 2001-032315/04.
XX
PT Isolated nucleic acid molecule encoding a human secreted protein is
PT used in preventing, treating or ameliorating a medical condition -
XX
PS Disclosure; Page 86; 506pp; English.
XX
CC Polynucleotide sequences AAF33095 - AAF33142 encode human secreted
CC proteins AAB64773 - AAB64820. Fragments of the secreted proteins and
CC amino acid sequences which share homology with the fragments are
CC represented in AAB64821 - AAB64880. The genes and proteins have
CC activities dependent on the tissues and cells in which they are
CC expressed. Examples of their activities and the activities of their
CC agonists and antagonists include; immunosuppressive; antiarthritic;
CC antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
CC cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
CC fungicide; and ophthalmological. The secreted proteins, polynucleotides,
CC antagonists and agonists may be useful in treating, preventing and
CC diagnosing diseases and disorders such as autoimmune diseases e.g.
CC rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the
CC breast or liver, cardiovascular disorders e.g. cardiac arrest,
CC cerebrovascular disorders e.g. cerebral ischemia, angiogenesis, nervous
CC system disorders e.g. Alzheimer's disease, infections caused by bacteria,
CC viruses and fungi and ocular disorders e.g. corneal infection. The
CC polypeptides can also be used to aid wound healing and epithelial cell
CC proliferation, to prevent skin aging due to sunburn, to maintain organs
CC before transplantation, for supporting cell culture of primary tissues,
CC to regenerate tissues and in chemotaxis. The polypeptides can also be
CC used as a food additive or preservative to increase or decrease storage
CC capabilities. Included in the invention are sequences AAB64772 and
CC AAF33095 - AAF33142 which are used in the isolation and characterisation
CC of the nucleotide and protein sequences of the invention.
XX
SQ Sequence 123 AA;

Query Match 49.2%; Score 123; DB 22; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.4e-111;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 128 KDSDVTEVMQPALRGRGLOAGYGVRIODAGVYLLYSQVLFQDVTFTMGQVVSREGQ 187
Db 1 KDSDVTEVMQPALRGRGLOAGYGVRIODAGVYLLYSQVLFQDVTFTMGQVVSREGQ 60
OY 188 GRQETLFR CIRSMPSHPDRAYNSCYAGVFHLHQGDILSVITIPARAKLNLSPHGTFLGF 247

Db 61 GRQETLFR CIRSMPSHPDRAYNSCYAGVFHLHQGDILSVITIPARAKLNLSPHGTFLGF 120
OY 248 VKL 250
Db 121 VKL 123

RESULT 37
AAW37003
ID AAW37003 standard; Protein; 168 AA.
XX
AC AAW37003;
XX
DT 14-APR-1998 (first entry)
XX
DE Human tumour necrosis factor epsilon.
XX
KW Human; tumour necrosis factor delta; TNF-delta; TNF-epsilon; cancer;
KW tumour necrosis factor epsilon; T cell proliferation;
KW immune regulation; inflammatory response.
XX
OS Homo sapiens.
XX
PN WO9733902-A1.
XX
PD 18-SEP-1997.
XX
PF 14-MAR-1996; 96WO-US03774.
XX
PR 14-MAR-1996; 96WO-US03774.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Gentz RL, Ni J, Yu G;
XX
DR WPI; 1997-470810/43.
DR N-PSDB; AAV00494.
XX
XX
PT Nucleic acid encoding human tumour necrosis factors delta and
PT epsilon - useful for destroying cancer cells, or mediating T cell
PT proliferation, immune regulation and inflammatory responses etc.
XX
PS Claim 20; Fig 2; 83pp; English.
XX
CC The present sequence represents human tumour necrosis factor (TNF)
CC epsilon. The TNF can be used to treat patients deficient in this factor
CC (optionally by in vivo expression). It is a ligand for TNF and can
CC destroy (by inducing apoptosis) some transformed cell lines (for tumour
CC treatment); mediate cell activity and proliferation (including T cells
CC to stimulate an immune response to viral, bacterial or parasitic
CC infections, also to eliminate autoreactive T cells in e.g. type I
CC diabetes), and is functionally linked as a primary mediator of immune
CC regulation and the inflammatory response. A typical application of the
CC protein, its agonists or antagonists is prevention of septic shock,
CC inflammation, cerebral malaria, human immunodeficiency virus activation,
CC graft-host reaction, bone resorption (osteoporosis), rheumatoid
CC arthritis and cachexia, also to promote wound healing (by upregulating
CC cell adhesion) and to regulate haematopoiesis. The protein can also be
CC used to isolate its cognate receptors (or receptor-encoding genes).
CC The cDNA can be used to produce recombinant proteins, and fragments of
CC it to isolate full-length or related sequences, for diagnostic detection
CC of mutations (indicative of disease or susceptibility) and for
CC chromosome identification. Analysis of patient samples for presence of
CC the new protein (e.g. using specific antibodies) can be used
CC diagnostically.
XX
SQ Sequence 168 AA;

Query Match 48.4%; Score 121; DB 18; Length 168;
Best Local Similarity 100.0%; Pred. No. 2.8e-109;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 130 DSDVTEVMQPALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFDQVTFMTMGQVVSREGQGR 189
|
Db 48 DSDVTEVMQPALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFDQVTFMTMGQVVSREGQGR 107

Oy 190 QETLFR CIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIPRARA KNLSPHGTF LGFVK 249
|
Db 108 QETLFR CIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIPRARA KNLSPHGTF LGFVK 167

Oy 250 L 250
|
Db 168 L 168

RESULT 38
AAU99509
ID AAU99509 standard; Protein; 168 AA.
XX
AC AAU99509;
XX
FT 07-OCT-2002 (first entry)
XX
KW Human tumour necrosis factor (TNF) epsilon #1.
KW Human; tumour necrosis factor; TNF epsilon; pulmonary system disorder;
KW immunoglobulin production; B-cell proliferation; immune system disorder;
KW autoimmune disease; cancer; lymphoproliferative disorder; pain;
KW microbial infection; parasitic infection; bone disease; atherosclerosis;
KW cardiovascular disorder; neurodegenerative disease; wound healing;
KW graft versus host disease; haematopoietic cell disorder; nephritis;
KW inflammatory disorder; mucous membrane disorder; dermatological;
KW immunosuppressive; cytostatic.
XX
OS Homo sapiens.
XX
PN US2002064829-A1.
XX
PD 30-MAY-2002.
XX
PF 14-JUN-2001; 2001US-0879919.
XX
PR 14-MAR-1996; 96US-016812P.
PR 15-JUN-2000; 2000US-211537P.
PR 23-OCT-2000; 2000US-241952P.
PR 13-DEC-2000; 2000US-254875P.
PR 16-MAR-2001; 2001US-276248P.
PR 23-MAR-2001; 2001US-277978P.
PR 25-MAY-2001; 2001US-293499P.
PR 12-MAR-1997; 97US-0815783.
XX
PI (HUMA-) HUMAN GENOME SCI INC.
PI Yu G, Ni J, Gentz RL, Dillon PJ;
XX
DR WPI; 2002-556722/59.
DR N-PSDB; ABK88684.
XX
PT Novel human multimeric tumour necrosis factor delta or epsilon protein
PT useful for treating disease or disorder of immune system such as
PT autoimmune disease, immunodeficiency, or cancer of immune system -
XX
PS Claim 1; Fig 2; 143pp; English.
XX
CC The present invention relates to the isolation of human tumour necrosis
CC factor (TNF) delta and TNF epsilon proteins, and the polynucleotide
CC sequences encoding them. The proteins are useful for modulating
CC immunoglobulin production or for modulating proliferation of B-cells.
CC The sequences of the invention are useful for treating diseases or
CC disorders of the immune system. Such disorders include autoimmune
CC diseases (e.g. systemic lupus erythematosus (SLE), acquired
CC immunodeficiency syndrome (AIDS)), cancers of the immune system
CC (e.g. chronic lymphocytic leukaemia (CLL), multiple myeloma,
CC non-Hodgkin's lymphoma or Hodgkin's disease), lymphoproliferative
CC disorders, microbial infections (e.g. viral, bacterial), parasitic

CC infections, nephritis, bone disease (e.g. osteoporosis), atherosclerosis,
CC pain, cardiovascular disorders (e.g. myocardial infarction, stroke),
CC neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's
CC disease), graft versus host disease, wound healing, haematopoietic cell
CC disorders (e.g. anaemia), inflammatory disorders (e.g. asthma),
CC diseases or disorders associated with various mucous membranes of the
CC body (e.g. mucositis), and disorders of the pulmonary system. The
CC proteins are also useful as a vaccine adjuvant that enhances immune
CC responsiveness to specific antigens. The present sequence represents
CC human TNF epsilon #1.
XX
SQ Sequence 168 AA;

Query Match 48.4%; Score 121; DB 23; Length 168;
Best Local Similarity 100.0%; Pred. No. 2.8e-109;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 130 DSDVTEVMQPALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFDQVTFMTMGQVVSREGQGR 189
|
Db 48 DSDVTEVMQPALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFDQVTFMTMGQVVSREGQGR 107

Oy 190 QETLFR CIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIPRARA KNLSPHGTF LGFVK 249
|
Db 108 QETLFR CIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIPRARA KNLSPHGTF LGFVK 167

Oy 250 L 250
|
Db 168 L 168

RESULT 39
AAU75403
ID AAU75403 standard; Protein; 168 AA.
XX
AC AAU75403;
XX
DT 09-APR-2002 (first entry)
XX
DE Tumour necrosis factor epsilon (TNF-epsilon), variant #1.
XX
DE Tumour necrosis factor epsilon; TNF-epsilon; cytostatic;
KW arteriosclerosis; analgesic; cerebroprotective; nootropic;
KW neuroprotective; hepatotropic; immunoglobulin production;
KW B cell proliferation; immunosuppressive; autoimmune disease; HIV;
KW human immunodeficiency virus; immunodeficiency; Sjogren's syndrome;
KW systemic lupus erythematosus; Hodgkin's disease;
KW common variable immunodeficiency; CVID; non-Hodgkin's lymphoma; AIDS;
KW acquired immunodeficiency virus; cancer; multiple myeloma; CLL;
KW chronic lymphocytic leukaemia; lymphoproliferative disorder;
KW bacterial infection; viral infection; osteoporosis; atherosclerosis;
KW pain; cardiovascular disorder; stroke; allergy; Alzheimer's disease;
KW neurodegenerative disease; inflammation; liver disease; cirrhosis;
KW cardiomyopathy; diabetes; asthma; psoriasis; glomerulonephritis;
KW ulcerative colitis; angiogenesis; septic shock; wound healing.
XX
OS Homo sapiens.
XX
FH Key location/Qualifiers
FH Peptide 1..38
FT /label= Signal_peptide
FT Protein 39..168
FT /label= Mature_TNF-epsilon
FT /note= "Tumour necrosis factor, specifically claimed
in claim 1"
FT Domain 10..17
FT /label= Conserved domain I
FT /note= "Region of high identity between TNF-delta
and TNF-epsilon"
FT Domain 47..56
FT /label= Conserved domain III
FT /note= "Region of high identity between TNF-delta
and TNF-epsilon"
FT Domain 61..74

FT	/label= Conserved domain IV
FT	/note= "Region of high identity between TNF-delta
FT	and TNF-epsilon"
FT	73..89
FT	/note= "TNF family signature sequence"
FT	79..89
FT	/label= Conserved domain V
FT	/note= "Region of high identity between TNF-delta
FT	and TNF-epsilon"
FT	101..111
FT	/label= Conserved domain VI
FT	/note= "Region of high identity between TNF-delta
FT	and TNF-epsilon"
FT	114..119
FT	/label= Conserved domain VII
FT	/note= "Region of high identity between TNF-delta
FT	and TNF-epsilon"
FT	126..130
FT	/label= Conserved domain VIII
FT	/note= "Region of high identity between TNF-delta
FT	and TNF-epsilon"
FT	133..144
FT	/label= Conserved domain IX
FT	/note= "Region of high identity between TNF-delta
FT	and TNF-epsilon"
FT	147..154
FT	/label= Conserved domain X
FT	/note= "Region of high identity between TNF-delta
FT	and TNF-epsilon"
FT	164..168
FT	/label= Conserved domain XI
FT	/note= "Region of high identity between TNF-delta
FT	and TNF-epsilon"

1 Yu G, Ni J, Gentz RL, Dillon PJ, Hilbert D;
XX
DR WPI; 2002-130727/17.
DR N-PSDB; ABK13402.
XX
PT Novel multimeric human tumour necrosis factor delta or epsilon protein
PT useful for treating cancer, immune system disorders, infection,
PT cardiovascular disorders, liver disease, cardiomyopathy, diabetes and
PT psoriasis -
XX
PS Claim 1; Fig 2A; 344pp; English.

The invention describes a multimeric human tumour necrosis factor (TNF) delta or epsilon protein (I). (I) or a composition containing them (II) are useful for modulating immunoglobulin production or proliferation of B cells. (I) or (II) is useful: for treating a disease or disorder of the immune system, preferably an autoimmune disease (e.g. Sjogren's syndrome, systemic lupus erythematosus or common variable immunodeficiency (CVID)); as an immunodeficiency e.g. acquired immunodeficiency syndrome (AIDS); cancer of the immune system (e.g. Hodgkin's disease, non-Hodgkin's lymphoma, multiple myeloma and chronic lymphocytic leukaemia (CLL)); in the diagnosis and treatment or prevention of cancer, lymphoproliferative disorder, bacterial and viral infections, osteoporosis, atherosclerosis, pain, cardiovascular disorders (e.g. stroke), allergy, inflammation,

neurodegenerative disease (e.g. Alzheimer's disease), liver disease (e.g. cirrhosis), cardiomyopathy, diabetes, asthma, psoriasis, septic shock, glomerulonephritis, ulcerative colitis, atherosclerosis; for promoting angiogenesis and wound healing; as a diagnostic research reagent; as an agent to target and kill cells expressing a TNFdelta and/or TNFepsilon receptor; in apoptosis of transformed cell lines; mediation of cell activation and proliferation; and as an immunogen to produce (II). (II) is useful to purify, detect and target (I), for measuring levels of (I) in biological samples, for immunophenotyping samples, and to treat, inhibit or prevent diseases and disorders associated with aberrant expression and/or activity of (I). This is the amino acid sequence of human tumour necrosis factor epsilon (TNF-epsilon) variant #1, described in the method of the invention.

SQ Sequence 168 AA;

Query Match	48.4%;	Score 121;	DB 23;	Length 168;
Best Local Similarity	100.0%;	Pred. No. 2.8e-109;		
Matches 121; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

```
QY      130 DSDVTEVMQPALRRGGLQAQGYSVRIQDAGVLLYSQVLFDQVTFTMGQVSREGQR   189
        |||||
Db       48 DSDVTEVMQPALRRRGQLAQSYSVRIQDAGVLLYSQVLFDQVTFTMGQVSREGQR   107
```

Qy 190 QETLFRICRSMSPHDPDAVNSCYSGAGVHLHQGDILSVIIPRAKAKLNSPHGTFGLGVK 249
108 QETLFRICRSMSPHDPDAVNSCYSGAGVHLHQGDILSVIIPRAKAKLNSPHGTFGLGVK 167

QY	250	L	250
Db	168	L	168

RESULT 40

AA128835 standard; Protein; 234 AA.

AC AAY28835

DT 17-JAN-2000 (first entry)

DE Human TNF-related death ligand-11.

KM Tumour necrosis factor-related death ligand-11; TRDL-11; cytokine;
KM TNF alpha; Fas ligand; FasL; TNF-related apoptosis-inducing ligand;
KM TRAIL; cellular apoptosis; transcription factor; NF kappa B; cancer;
KM autoimmune disease; viral infection; antagonist; AIDS; probe; primer;
KM neurodegenerative disease; myelodysplastic disease; ischaemic injury;
KM chromosome localisation; antibody.

OS Homo sapiens.

FH	Key	Location/Qualifiers
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
9	9	9
10	10	10
11	11	11
12	12	12
13	13	13
14	14	14
15	15	15
16	16	16
17	17	17
18	18	18
19	19	19
20	20	20
21	21	21
22	22	22
23	23	23
24	24	24
25	25	25
26	26	26
27	27	27
28	28	28
29	29	29
30	30	30
31	31	31
32	32	32
33	33	33
34	34	34
35	35	35
36	36	36
37	37	37
38	38	38
39	39	39
40	40	40
41	41	41
42	42	42
43	43	43
44	44	44
45	45	45
46	46	46
47	47	47
48	48	48
49	49	49
50	50	50
51	51	51
52	52	52
53	53	53
54	54	54
55	55	55
56	56	56
57	57	57
58	58	58
59	59	59
60	60	60
61	61	61
62	62	62
63	63	63
64	64	64
65	65	65
66	66	66
67	67	67
68	68	68
69	69	69
70	70	70
71	71	71
72	72	72
73	73	73
74	74	74
75	75	75
76	76	76
77	77	77
78	78	78
79	79	79
80	80	80
81	81	81
82	82	82
83	83	83
84	84	84
85	85	85
86	86	86
87	87	87
88	88	88
89	89	89
90	90	90
91	91	91
92	92	92
93	93	93
94	94	94
95	95	95
96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

/label= N-terminal_cytoplasmic_domain

```
FT /label= Transmembrane_domain
```

```
FT      /label= C-terminal_extracellular_domain
```

PN W09950416-A1.

PD 07-OCT-1999.

PF 21-SEP-1998; 98WO-US18506.

PR 30-SEP-1997; 97US-0060475.

PA (PHAA) PHARMACIA & UPJOHN CO.

PI Bienkowski MJ, Jones DA, Mills CJ;

DR WPI; 1999-610854/52.

DR N-PSDB; MAX90910.
XX
PT New nucleic acid used for promotion or inhibition of apoptosis, e.g.
PT for treating cancer -
XX
PS Claim 1; Fig 3; 70pp; English.
XX
CC The present sequence is tumour necrosis factor (TNF)-related death
CC ligand-11 (TRDL-11), that belongs to the C-terminal domain of TNF alpha, Fas
CC and 12% sequence homology to the C-terminal domain of TNF alpha, Fas
CC ligand (FasL) and TNF-related apoptosis-inducing ligand (TRAIL)
CC respectively. It can activate cellular apoptosis and transcription factor
CC NF kappa B and can be used for treating conditions associated with
CC inadequate levels of apoptosis, like cancer, autoimmune disease and viral
CC infections. TRDL antagonist can be used to reduce apoptosis levels in
CC conditions like, AIDS, neurodegenerative diseases, myelodysplastic
CC disease and ischaemic injury. TRDL gene can be used for chromosome
CC localisation and as probe or primer for detecting TRDL nucleic acid or
CC cells that express TRDL. Antibodies generated against TRDL are useful for
CC detecting TRDL expression.

Sequence 234 AA;

Query Match 48.4%; Score 121; DB 20; Length 234;
Best Local Similarity 100.0%; Pred. No. 3.7e-109;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 DSDVTEVMQPALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQVVSREGQGR 189
|||
Db 114 DSDVTEVMQPALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQVVSREGQGR 173

QY 190 QETLFR CIRSMPSHPDRAYNSCYAGVPHLHOGDILSVIIPRARA KNLNSPHGTF LGFVK 249
|||
Db 174 QETLFR CIRSMPSHPDRAYNSCYAGVPHLHOGDILSVIIPRARA KNLNSPHGTF LGFVK 233

QY 250 L 250
|
Db 234 L 234

RESULT 41
AAB62330
ID AAB62330 standard; protein; 234 AA.

AC AAB62330;
XX
DT 29-JUN-2001 (first entry)

Human TRDL-1beta polypeptide.

KW Tumour necrosis factor related death ligand-1gamma; TRDL-1gamma; TRDL;
KW cell death; apoptosis; human; TRDL-1beta.

OS Homo sapiens.
XX
PN WO200125256-A2.

PD 12-APR-2001.

PF 06-OCT-2000; 2000WO-US27868.

PR 06-OCT-1999; 99US-0157913.

PA (UTAH) UNIV UTAH RES FOUND.

PI Jones D, Manos E;

DR WPI; 2001-281728/29.

PT Isolated and purified polynucleotide encoding human tumor necrosis
PT factor related death ligand (TRDL)-1 gamma useful for identifying
PT agents that inhibit or enhance TRDL-1 gamma mediated induction of
PT apoptosis -

XX Disclosure; Fig 1; 39pp; English.
PS
XX
CC The invention provides a human tumour necrosis factor related death
CC ligand-1gamma (TRDL-1gamma). The TRDL-1gamma polypeptide can be
CC expressed by standard recombinant methodology. TRDL-1gamma stimulates
CC Jurkat cell death. It is useful for identifying agents capable of
CC inhibiting or enhancing TRDL-1gamma mediated induction of apoptosis.
CC The present sequence represents a TRDL-1beta polypeptide, used in
CC alignment studies.

SQ Sequence 234 AA;

Query Match 48.4%; Score 121; DB 22; Length 234;
Best Local Similarity 100.0%; Pred. No. 3.7e-109;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 DSDVTEVMQPALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQVVSREGQGR 189
|||
Db 114 DSDVTEVMQPALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQVVSREGQGR 173

QY 190 QETLFR CIRSMPSHPDRAYNSCYAGVPHLHOGDILSVIIPRARA KNLNSPHGTF LGFVK 249
|||
Db 174 QETLFR CIRSMPSHPDRAYNSCYAGVPHLHOGDILSVIIPRARA KNLNSPHGTF LGFVK 233

QY 250 L 250
|
Db 234 L 234

RESULT 42

AAU99511
ID AAU99511 standard; protein; 234 AA.

AC AAU99511;

DT 07-OCT-2002 (first entry)

DE Human tumour necrosis factor (TNF) epsilon #2.

KW Human; tumour necrosis factor; TNF epsilon; pulmonary system disorder;
KW immunoglobulin production; B-cell proliferation; immune system disorder;
KW autoimmune disease; cancer; lymphoproliferative disorder; pain;
KW microbial infection; parasitic infection; bone disease; atherosclerosis;
KW cardiovascular disorder; neurodegenerative disease; wound healing;
KW graft versus host disease; haematopoietic cell disorder; nephritis;
KW inflammatory disorder; mucous membrane disorder; dermatological;
KW immunosuppressive; cytostatic.

OS Homo sapiens.

PN US2002064829-A1.

PD 30-MAY-2002.

PF 14-JUN-2001; 2001US-0879919.

PR 14-MAR-1996; 96US-016812P.

PR 15-JUN-2000; 2000US-211537P.

PR 23-OCT-2000; 2000US-241952P.

PR 13-DEC-2000; 2000US-254875P.

PR 16-MAR-2001; 2001US-276248P.

PR 23-MAR-2001; 2001US-27978P.

PR 25-MAY-2001; 2001US-293499P.

PR 12-MAR-1997; 97US-0815783.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Yu G, Ni J, Gentz RL, Dillon PJ;

DR WPI; 2002-556722/59.

DR N-PSDB; ABK88689.

PT psoriasis -
XX
PS Claim 1; Fig 7A-B; 344pp; English.
XX
CC The invention describes a multimeric human tumour necrosis factor (TNF)
CC delta or epsilon protein (I). (I) or a composition containing them (II)
CC are useful for modulating immunoglobulin production or proliferation of B
CC cells. (I) or (II) is useful for treating a disease or disorder of the
CC immune system, preferably an autoimmune disease (e.g. Sjogren's syndrome,
CC systemic lupus erythematosus or common variable immunodeficiency (CVID));
CC an immunodeficiency e.g. acquired immunodeficiency syndrome (AIDS);
CC cancer of the immune system (e.g. Hodgkin's disease, non-Hodgkin's
CC lymphoma, multiple myeloma and chronic lymphocytic leukaemia (CLL)); in
CC the diagnosis and treatment or prevention of cancer, lymphoproliferative
CC disorder, bacterial and viral infections, osteoporosis, atherosclerosis,
CC pain, cardiovascular disorders (e.g. stroke), allergy, inflammation,
CC neurodegenerative disease (e.g. Alzheimer's disease), liver disease (e.g.
CC cirrhosis), cardiomyopathy, diabetes, asthma, psoriasis, septic shock,
CC glomerulonephritis, ulcerative colitis, arteriosclerosis; for promoting
CC angiogenesis and wound healing; as a diagnostic research reagent; as an
CC agent to target and kill cells expressing a TNFdelta and/or TNFepsilon
CC receptor; in apoptosis of transformed cell lines; mediation of cell
CC activation and proliferation; and as an immunogen to produce (II). (II)
CC is useful to purify, detect and target (I), for measuring levels of (I)
CC in biological samples, for immunophenotyping samples, and to treat,
CC inhibit or prevent diseases and disorders associated with aberrant
CC expression and/or activity of (I). This sequence encodes human tumour
CC necrosis factor epsilon (TNF-epsilon) variant #2, described in the
CC method of the invention.
XX
SQ Sequence 234 AA;

Query Match 48.4%; Score 121; DB 23; Length 234;
Best Local Similarity 100.0%; Pred. No. 3.7e-109;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 DSDVTEVMQPALRRGRLQAGYGVRIQDAGVYLLYSQVLFQDVTFTMGQVVSREGQGR 189
DB 114 DSDVTEVMQPALRRGRLQAGYGVRIQDAGVYLLYSQVLFQDVTFTMGQVVSREGQGR 173
QY 190 QETLFR CIRSMPSHPDRAYNSCYSGVFLHOGDILSVIIPRAKLNLSPHGTFLGFKV 249
DB 174 QETLFR CIRSMPSHPDRAYNSCYSGVFLHOGDILSVIIPRAKLNLSPHGTFLGFKV 233
QY 250 L 250
DB 234 L 234

RESULT 44
ID AAY74026 standard; Protein; 244 AA.
AC AAY74026;
DT 14-MAR-2000 (first entry)
XX
DE Human prostate tumor EST fragment derived protein #213.
XX
KW Pancreas; tumor; EST; expressed sequence tag; human; cytostatic;
KW treatment.
XX
OS Homo sapiens.
XX
PN DE19820190-A1.
XX
PD 04-NOV-1999.
XX
PF 28-APR-1998; 98DE-1020190.
XX
PR 28-APR-1998; 98DE-1020190.
XX
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.

XX
PI Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;
XX
DR WPI; 1999-621386/54.
DR N-PSDB; AAZ52928.
XX
PT New human nucleic acid sequences from pancreatic tumors, and related
PT proteins -
XX
PS Claim 23; Page 398; 502pp; German.
XX
CC This invention describes novel polypeptides and their encoding nucleic
CC acids derived from human pancreatic tumor tissue which have cytostatic
CC activity. The sequences are also useful in producing pharmaceutical
CC compositions for treatment of pancreatic tumors. AAY73814-Y74252
CC represent protein fragments encoded by the human pancreatic tumor cDNA
CC library derived expressed sequence tag (EST) sequences represented in
CC AAZ52858-253014.
XX
SQ Sequence 244 AA;

Query Match 48.4%; Score 121; DB 20; Length 244;
Best Local Similarity 100.0%; Pred. No. 3.8e-109;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 DSDVTEVMQPALRRGRLQAGYGVRIQDAGVYLLYSQVLFQDVTFTMGQVVSREGQGR 189
DB 124 DSDVTEVMQPALRRGRLQAGYGVRIQDAGVYLLYSQVLFQDVTFTMGQVVSREGQGR 183
QY 190 QETLFR CIRSMPSHPDRAYNSCYSGVFLHOGDILSVIIPRAKLNLSPHGTFLGFKV 249
DB 184 QETLFR CIRSMPSHPDRAYNSCYSGVFLHOGDILSVIIPRAKLNLSPHGTFLGFKV 243
QY 250 L 250
DB 244 L 244

RESULT 45
ID AAE15499 standard; Protein; 149 AA.
AC AAE15499;
XX
DT 12-MAR-2002 (first entry)
XX
DE Mouse FLAG-tagged soluble G70 protein.
XX
KW Mouse; transmembrane activator and intracellular CAML interactor; TACT;
KW cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KW rheumatoid arthritis; atherosclerosis; G70 protein.
XX
OS Mus sp.
OS Synthetic.
XX
PN WO200187979-A2.
XX
PD 22-NOV-2001.
XX
PF 14-MAY-2001; 2001WO-US15567.
XX
PR 12-MAY-2000; 2000US-204039P.
PR 27-JUN-2000; 2000US-214591P.
PR 14-MAY-2001; 2001US-0214591.
XX
PA (AMGE-) AMGEN INC.
XX
PI Theill LE, Yu G;

XX WPI; 2002-066686/09.
DR
XX
PT Inhibiting activity of B cell maturation protein and/or transmembrane
PT activator and intracellular cyclophilin ligand interactor, by
PT administering a binding partner for APRIL, a tumor necrosis factor
PT family ligand
XX
PS Disclosure; Fig 2B; 94pp; English.
XX
CC The invention relates to a method for inhibiting TACI (transmembrane
CC activator and intracellular CAML interactor) and/or B cell maturation
CC protein (BCMA) activity in a mammal. The method comprises administering
CC a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
CC BCMA extracellular consensus sequence, but not the extracellular region
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC lymphoproliferative disorders, one or more solid tumours such as lung,
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung,
CC disease), drug and insect sting allergy, inflammatory bowel disease
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC with leucocyte infiltration of the skin or organs. The present sequence
CC is mouse FLAG-tagged soluble G70 protein.
XX
SQ Sequence 149 AA;
Query Match 8.4%; Score 21; DB 23; Length 149;
Best Local Similarity 100.0%; Pred. No. 3.3e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 204 PDRAYNSCYSAGVFHLHGDI 224
Db 103 PDRAYNSCYSAGVFHLHGDI 123
RESULT 46
AAO14137
ID AAO14137 standard; Protein; 176 AA.
XX
AC AAO14137;
XX
02-MAY-2002 (first entry)
DB Protein of a FLAG-tagged soluble extracellular domain of murine APRIL.
XX
KM Human transmembrane activator CAML interactor protein; TACI; cytostatic;
KM cell proliferation; tumour; vulnery; renal cell cancer; mastocytoma;
KM Kaposi's sarcoma; breast; ovarian carcinoma; rectal; throat; melanoma;
KM colon; bladder; mammary adenocarcinoma; gastrointestinal; hyperplasia;
KM pharyngeal squamous cell; stomach; cellular hyperproliferation; pannus;
KM scleroderma; rheumatoid arthritis; scarring; mean survival time; liver;
KM lung fibrosis; uterine; murine; a proliferation inducing ligand; mouse;
KM APRIL; PS784; LT032.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Peptide 1..15 /note= "NA signal sequence"
FT 16..23 /note= "FLAG epitope"
FT Region 24..31 /note= "Short linker sequence, linking the FLAG epitope
FT to the soluble murine APRIL sequence"
FT 32..176 /note= "Murine APRIL sequence"
XX

PN WO200181417-A2.
XX
PD 01-NOV-2001.
XX
XX 27-APR-2001; 2001WO-US40626.
PF
XX 27-APR-2000; 2000US-199946P.
PR
XX
PA (BIOJ) BIOGEN INC.
PA (APOT-) APOTEC R & D SA.
PI Ambrose C, Thompson J, Schneider P, Rennert P;
XX
DR WPI; 2002-062027/08.
XX N-PSDB; AAK98733.
PT Treating mammal for condition associated with undesired cell
PT proliferation e.g., solid tumour or reducing solid tumour size located in
PT mammal comprises administering transmembrane activator CAML interactor
PT protein reagent -
XX
PS Examples; Fig 7; 42pp; English.
XX
CC This sequence represents the protein encoded by the DNA of a FLAG-tagged
CC soluble extracellular domain of murine APRIL (A Proliferation Inducing
CC ligand) as mapped in the mammalian expression plasmid PS784, also known
CC as LT032. The invention relates to treating a mammal for a condition
CC associated with undesired cell proliferation (e.g. a solid tumour, or
CC reducing the size of a solid tumour located on or in a mammal) comprising
CC administering a transmembrane activator CAML interactor protein (TACI)
CC reagent. The TACI reagent has cytostatic and vulnery activity. Treating
CC a mammal (e.g. human, cow, horse, dog, mouse, rat or cat) for a condition
CC associated with undesired cell proliferation (e.g. cancer such as renal
CC cell cancer, Kaposi's sarcoma, breast cancer, sarcoma, ovarian carcinoma,
CC rectal cancer, throat cancer, melanoma, colon cancer, bladder cancer,
CC mastocytoma, lung cancer, mammary adenocarcinoma, pharyngeal squamous
CC cell carcinoma, gastrointestinal cancer or stomach cancer). The method is
CC also useful for treating cellular hyperproliferation (hyperplasia) such
CC as scleroderma, pannus formation in rheumatoid arthritis, post-surgical
CC scarring and lung, liver and uterine fibrosis. The TACI reagent of the
CC invention can extend mean survival time of a mammal by 25% as compared to
CC the mean survival time of a mammal in the absence of administering the
CC TACI reagent. The TACI reagent also reduces the size of the tumour by 25%
CC or more.
XX
SQ Sequence 176 AA;
Query Match 8.4%; Score 21; DB 23; Length 176;
Best Local Similarity 100.0%; Pred. No. 3.8e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 204 PDRAYNSCYSAGVFHLHGDI 224
Db 130 PDRAYNSCYSAGVFHLHGDI 150
RESULT 47
AAE15503
ID AAE15503 standard; Protein; 199 AA.
XX
AC AAE15503;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human-mouse APRIL G70 protein consensus sequence.
XX
KM Human; transmembrane activator and intracellular CAML interactor; TACI;
KM cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
KM lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KM prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KM drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KM Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KM human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;

KW rheumatoid arthritis; atherosclerosis; APRIL G70.
XX
OS Homo sapiens.
OS Mus sp.
XX
PN WO200187979-A2.
XX
PD 22-NOV-2001.
XX
PF 14-MAY-2001; 2001WO-US15567.
XX
PR 12-MAY-2000; 2000US-204039P.
PR 27-JUN-2000; 2000US-214591P.
PR 14-MAY-2001; 2001US-0214591.
XX
PA (AMGE-) AMGEN INC.
XX
PI The111 LE, Yu G;
XX
PS WPI; 2002-066686/09.
XX
PT Inhibiting activity of B cell maturation protein and/or transmembrane
PT activator and intracellular cyclophilin ligand interactor, by
PT administering a binding partner for APRIL, a tumor necrosis factor
PT family ligand
XX
PS Disclosure; Fig 3; 94pp; English.
XX
CC The invention relates to a method for inhibiting TACI (transmembrane
CC activator and intracellular CAML interactor) and/or B cell maturation
CC protein (BCMA) activity in a mammal. The method comprises administering
CC a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
CC BCMA extracellular consensus sequence, but not the extracellular region
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC lymphoproliferative disorders, one or more solid tumours such as lung,
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
CC disease), drug and insect sting allergy, inflammatory bowel disease
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC with leucocyte infiltration of the skin or organs. The present sequence
CC is human-mouse APRIL G70 protein consensus sequence.

Sequence 199 AA;
Query Match 8.4%; Score 21; DB 23; Length 199;
Best Local Similarity 100.0%; Pred. No. 4.2e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 204 PDRAYNSCYSAGVFHLHQGDI 224
Db 158 PDRAYNSCYSAGVFHLHQGDI 178

RESULT 48
AAAY04284
ID AAY04284 standard; Protein; 232 AA.
XX
AC AAY04284;
XX
DT 17-JUN-1999 (first entry)
XX
DE Mouse APRIL protein sequence.
XX
KW APRIL; tumour necrosis factor; TNF; proliferating inducing agent;
KW immune disorder; cancer.
XX
OS Mus sp.

XX
PN WO9912965-A2.
XX
PD 18-MAR-1999.
XX
PF 11-SEP-1998; 98WO-US19191.
XX
PR 26-MAR-1998; 98US-0079384.
PR 12-SEP-1997; 97US-0058786.
XX
PA (BIOJ) BIOGEN INC.
XX
PI Tschopp J;
XX
DR WPI; 1999-215028/18.
DR N-PSDB; AAX30125.
XX
PT A Proliferating Inducing Agent (APRIL), a member of the Tumour
PT Necrosis Factor Family - useful as diagnostic agents and for
PT prevention or treatment of immune disorders and cancer
XX
PS Disclosure; Page 47; 47pp; English.
XX
CC The present sequence represents a proliferating inducing agent (APRIL)
CC isolated from mouse. APRIL is a member of the tumour necrosis factor
CC family, and essentially free of normally associated proteins. APRIL and
CC APRIL antibodies are useful in pharmaceutical compositions for
CC preventing or reducing severity of an autoimmune disease or an immune
CC response to tissue graft. The composition is also useful for stimulating
CC or suppressing the immune system, and treating cancer. APRIL is also
CC useful for treating APRIL-related disorders by delivering via a vector
CC (preferably viral vector) (gene therapy) into a mammalian (preferably
CC human) cell. Labeled APRIL and fragments are useful for identifying
CC APRIL receptors by screening compositions. Antisense DNA and antibodies
CC and modified APRIL (preferably an anti-APRIL receptor antibody) are
CC useful as blocking agents for inducing cell death by interfering with
CC APRIL receptors. The blocking agent is preferably administered with
CC interferon-c, and treats, suppresses or alters an immune response
CC involving a signalling pathway between APRIL and its receptor
CC (preferably involving human carcinoma cells); and also treats,
CC suppresses or alters the progression of cancer (preferably at least one
CC chemotherapeutic agent is also administered, and radiation therapy is
CC also given to the patient.

Sequence 232 AA;
Query Match 8.4%; Score 21; DB 20; Length 232;
Best Local Similarity 100.0%; Pred. No. 4.8e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 204 PDRAYNSCYSAGVFHLHQGDI 224
Db 186 PDRAYNSCYSAGVFHLHQGDI 206

RESULT 49
AAAY79672
ID AAY79672 standard; Protein; 232 AA.
XX
AC AAY79672;
XX
DT 29-AUG-2000 (first entry)
XX
DE Mouse death receptor ligand-1 (DRL-1).
XX
KW DRL-1; mouse; death receptor ligand-1; tumour necrosis factor;
KW TNF-gamma; TNF-like ligand; TLL; immunostimulant; immunosuppressive;
KW T-cell response; transplant rejection; graft versus host disease;
KW apoptosis.
XX
OS Mus sp.
XX
PN WO200026244-A2.

XX PD 11-MAY-2000.
XX PF 04-NOV-1999; 99WO-US25954.
XX PR 04-NOV-1998; 98US-0106976.
XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX PI Leonardo MJ, Wang J, Jiang D;
XX DR WPI; 2000-365575/31.
XX DR N-PSDB; AAA27734.
XX PT Novel nucleic acids encoding tumor necrosis factor family polypeptides
XX PT termed as Death Receptor Ligands useful for stimulating immune response
XX PT and inducing apoptosis comprising a specific nucleotide sequence -
XX PS Claim 20; Page 77; 80pp; English.
XX CC The present sequence is that of mouse death receptor ligand 1
XX CC (DRL-1), a novel member of the tumor necrosis factor (TNF) family,
XX CC also termed TNF-gamma or TNF-like ligand (TLL). The invention
XX CC provides human and murine DRL polypeptides, nucleic acids and
XX CC antibodies. DRL-1 polypeptides are used in claimed methods of
XX CC stimulating an immune response and of inducing apoptosis in a
XX CC population of T-cells. Antibodies to DRL-1 are used in claimed
XX CC methods of suppressing an immune response, inhibiting a T-cell
XX CC response associated with transplant rejection or graft versus host
XX CC disease, inhibiting apoptosis in a population of T cells, and of
XX CC stimulating the membrane-bound form of DRL-1.
XX SQ Sequence 232 AA;
OY Query Match 8.4%; Score 21; DB 21; Length 232;
Best Local Similarity 100.0%; Pred. No. 4.8e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 204 PDRAYNSCYSAGVFHLHQDI 224
186 PDRAYNSCYSAGVFHLHQDI 206
RESULT 50
AAE07878 ID AAE07878 standard; Protein; 232 AA.
XX AC AAE07878;
XX 01-NOV-2001 (first entry)
XX DE Mouse APRIL protein.
XX KW Mouse; tumour necrosis factor; TNF; APBF; APRIL; BAF; therapy; melanoma;
KW immune system-related disorder; cancer; renal cell; breast; stomach;
KW rectal; colon; throat; bladder; ovarian carcinoma; cellular disorder;
KW gastrointestinal; scleroderma; Kaposi's sarcoma; chronic leukaemia;
KW squamous cell carcinoma; hyperproliferative condition; pannus formation;
KW rheumatoid arthritis; postsurgical scarring; fibrosis; liver; uterine;
KW lung; immunodeficiency; inflammatory disease; lymphadenopathy; vulnery;
KW autoimmune disease; graft versus host disease; dermatological;
KW antiinflammatory; immunosuppressive; cytostatic.
XX OS Mus sp.
XX FH Key Location/Qualifiers
FT Misc-difference 133 /note= "Encoded by CCA"
FT Misc-difference 134..135
FT /note= "Encoded by GGGAGAC"
XX PN WO200158949-A2.
XX

XX PD 16-AUG-2001.
XX PF 08-FEB-2001; 2001WO-US04121.
XX PR 11-FEB-2000; 2000US-0181670.
XX PA (BIOJ) BIOGEN INC.
XX PI Rennert PD, Thompson JS, Ambrose C, Cachero TG;
XX DR WPI; 2001-514644/56.
XX DR N-PSDB; AAD14416.
XX PT New heteromeric ligand of tumor necrosis factor (TNF) family, useful
XX PT for diagnosis, treatment of immune system-related disorders in humans,
XX PT comprises TNF-family member APRIL subunit linked non-covalently to
XX PT TNF-family member BAF subunit -
XX PS Claim 2; Fig 1e; 42pp; English.
XX CC The present invention relates to an isolated heteromeric ligand of
XX CC tumor necrosis factor (TNF)-family, referred to as APBF comprising a
XX CC TNF-family member APRIL subunit linked non-covalently to TNF-family
XX CC member BAF subunit. APBF is useful for diagnosis or treatment of
XX CC various immune system-related disorders in mammals, preferably humans.
XX CC Such disorders include cancer, including cellular disorders, for e.g.
XX CC renal cell cancer, Kaposi's sarcoma, chronic leukaemia, breast cancer,
XX CC sarcoma, ovarian carcinoma, rectal cancer, throat cancer, melanoma,
XX CC colon cancer, bladder cancer, squamous cell carcinoma and
XX CC gastrointestinal or stomach cancer, cellular hyperproliferative
XX CC conditions, such as scleroderma, pannus formation in rheumatoid
XX CC arthritis, postsurgical scarring and lung, liver and uterine fibrosis
XX CC and immunodeficiencies, inflammatory diseases, lymphadenopathy,
XX CC autoimmune diseases and graft versus host disease. APBF is also useful
XX CC for producing monoclonal or polyclonal antibodies and for identifying
XX CC novel modulators affecting biological function and receptors interacting
XX CC with APBF. The present sequence is mouse APRIL protein.
XX SQ Sequence 232 AA;
OY Query Match 8.4%; Score 21; DB 22; Length 232;
Best Local Similarity 100.0%; Pred. No. 4.8e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 204 PDRAYNSCYSAGVFHLHQDI 224
186 PDRAYNSCYSAGVFHLHQDI 206
RESULT 51
AAE00504 ID AAE00504 standard; Protein; 234 AA.
XX AC AAE00504;
XX 31-JUL-2001 (first entry)
XX DE Murine myc tagged A Proliferation Inducing Ligand (APRIL).
XX KW Murine: A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;
KW gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;
KW carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;
KW systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;
KW B-cell lympho-proliferative disorder; BCM; immunosuppressive virus;
KW organ transplantation; KEL motif; HIV; human immunodeficiency virus;
KW tumour necrosis factor; TNF; BCMA; B cell maturation protein; myc tag.
XX OS Mus sp.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Region 86..96
FT /label= Myc_tag
FT

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FT      Domain      .      97..99
FT      /label= KEL_motif
FT      /note= "This motif is from FAS ligand"
XX      PN      WO200124811-A1.
XX      PD      12-APR-2001.
XX      PF      05-OCT-2000; 2000WO-US27579.
XX      PR      06-OCT-1999; 99US-0157933.
XX      PR      11-FEB-2000; 2000US-0181807.
XX      PR      30-JUN-2000; 2000US-0215688.
XX      PA      (BIOJ ) BIOGEN INC.
XX      PA      (APOT-) APOTTECH R & D SA.
XX      PI      Schneider P, Thompson J, Cachero T, Ambrose C, Rennert P;
XX      PI      MPI; 2001-266242/27.
XX      PS      N-PSDB; AAD03840.
XX      PT      Treating a mammal for a condition associated with undesired cell
XX      PT      proliferation such as cancer or carcinoma, comprises administering a
XX      PT      composition comprising A Proliferation Inducing Ligand Receptor
XX      PT      (APRIL-R) antagonist -
XX      PS      Example 1; Fig 1; 85pp; English.
XX      PS
XX      CC      The invention relates to a method of treating a mammal for a condition
XX      CC      associated with undesired cell proliferation such as cancer or
XX      CC      carcinoma. The method involves administering a composition comprising
XX      CC      A Proliferation Inducing Ligand Receptor (APRIL-R) also referred as
XX      CC      B cell maturation protein (BCM or BCMA) antagonist that antagonises the
XX      CC      interaction between APRIL and its cognate receptor(s). This method is
XX      CC      useful for treating undesired cell proliferation such as cancer or
XX      CC      carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,
XX      CC      prostate carcinoma, and other carcinomas whose proliferation is modulated
XX      CC      by APRIL. It is also useful for treating autoimmune diseases (Grave's
XX      CC      disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular
XX      CC      diseases, renal disorders, B-cell lympho-proliferative disorders,
XX      CC      immunosuppressive diseases, organ transplantation, inflammation and
XX      CC      human immunodeficiency virus (HIV), and for treating, suppressing or
XX      CC      altering an immune response involving a signalling pathway between
XX      CC      APRIL-R and its ligand. APRIL-R DNA is also useful in gene therapy.
XX      CC      The present sequence is murine A Proliferation Inducing Ligand (APRIL)
XX      CC      protein. This sequence comprises myc epitope and KEL motif from FAS
XX      CC      ligand followed by APRIL extracellular domain. APRIL is a member of
XX      CC      Tumour Necrosis Factor (TNF) family of proteins.
XX      SS      Sequence      234 AA;
XX      SS
XX      SS      Query Match      8.4%; Score 21; DB 22; Length 234;
XX      SS      Best Local Similarity      100.0%; Pred. NO. 4.9e-12;
XX      SS      Matches      21; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
XX      SS
XX      SS      QY      204      PDRAYNSCYSGVFHLHOGDI      224
XX      SS      |||||||||||||||||||
XX      SS      DB      188      PDRAYNSCYSGVFHLHOGDI      208
XX      SS
XX      SS      RESULT 52
XX      SS      ID      AAE15483 standard; Protein; 240 AA.
XX      SS      AC      AAE15483;
XX      SS      DT      12-MAR-2002 (first entry)
XX      SS      DE      Mouse APRIL/G70 protein.
XX      SS
XX      KW      Mouse; transmembrane activator and intracellular CAML interactor; TACI;
XX      KW      cyostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;

```

KW	lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KW	prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KW	drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KW	Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KW	human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KW	rheumatoid arthritis; atherosclerosis; APRIL G70.
XX	
OS	Mus sp.
XX	
PN	WO200187979-A2.
XX	
PD	22-NOV-2001.
XX	
PF	14-MAY-2001; 2001WO-US15567.
XX	
PR	12-MAY-2000; 2000US-204039P.
PR	27-JUN-2000; 2000US-214591P.
XX	
PA	14-MAY-2001; 2001US-0214591.
XX	
PI	(AMGE-) AMGEN INC.
XX	
PI	Theill LE, Yu G;
XX	
DR	WPI; 2002-066686/09.
DR	N-PSDB; AAD24709.
XX	
PT	Inhibiting activity of B cell maturation protein and/or transmembrane
PT	activator and intracellular cyclophilin ligand interactor, by
PT	administering a binding partner for APRIL, a tumor necrosis factor
PT	family ligand -
XX	
PS	Disclosure; Fig 2B; 94pp; English.
XX	
CC	The invention relates to a method for inhibiting TACI (transmembrane
CC	activator and intracellular CAML interactor) and/or B cell maturation
CC	protein (BCMA) activity in a mammal. The method comprises administering
CC	a specific binding partner for APRIL (G70, a tumor necrosis factor-TNF
CC	family ligand), having the consensus region of TACI, BCMA, or the TACI/
CC	BCMA extracellular consensus sequence, but not the extracellular region
CC	of TACI or BCMA. The method is useful for inhibiting activity of TACI
CC	and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC	lymphoproliferative disorders, one or more solid tumours such as lung,
CC	gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
CC	antagonists are useful for treating inflammation and immune function
CC	diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC	dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
CC	disease), drug and insect sting allergy, inflammatory bowel disease
CC	(Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
CC	sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
CC	bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC	with leucocyte infiltration of the skin or organs. The present sequence
CC	is mouse APRIL G70 protein.
XX	
SQ	Sequence 240 AA;
QY	Query Match 8.4%; Score 21; DB 23; Length 240;
	Best Local Similarity 100.0%; Pred. No. 5e-12;
	Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB	204 PDRAYNSCYSAQVPHLHOGDI 224
	194 PDRAYNSCYSAQVPHLHOGDI 214
RESULT 53	
ID	AAW93589 standard; Protein; 241 AA.
XX	
AC	AAW93589;
XX	
DT	18-JUN-1999 (first entry)
XX	
DE	Mouse TNRL1-beta protein.

```
XX Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;  
KW developmental abnormality; gestational abnormality; prostate cancer;  
KW APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;  
KM cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;  
XW apoptosis; mouse; TNRL1-beta.  
XX  
OS Mus sp.  
XX WO911791-A2.  
PN  
XX 11-MAR-1999.  
PD  
XX 04-SEP-1998; 98WO-US18393.  
PF  
XX 05-SEP-1997; 97US-0924634.  
PR  
XX (UNIW ) UNIV WASHINGTON.  
PA Chaudhary PM;  
XX  
DR MPI; 1999-205191/17.  
DR N-PSDB; AA23423.  
PT  
PP New Tumor Necrosis Factor family receptor polypeptides and ligands -  
developmental or gestational abnormalities  
PT  
XX  
PS Claim 35; Fig 12B; 156pp; English.  
XX  
XX This invention describes isolated Tumor Necrosis Factor (TNF) family  
receptor polypeptides: APO4, APO6, APO8 and APO9 or their active  
fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or  
their active fragments. APO4 is useful for diagnosing prostate cancer  
by determining levels of APO4 in an individual. Prostate cancer can also  
be treated using APO4 selective binding agents linked to a therapeutic  
moiety. APO4 polypeptides are also useful for identifying selective  
binding agents, useful in diagnosis/treatment of disease by binding of  
agents to the polypeptide/active fragment which is extracellular, or  
expressed on the cell surface. The binding is preferably performed in  
vivo. APO4 polypeptides/ active fragments are also useful for screening  
for agonists and antagonists by binding and observing the change in APO4  
activity. Effective pharmacological agents useful in diagnosis or  
treatment of disease are also identified using APO4 polypeptides/active  
fragments and APO4 signal transducer molecules that specifically interact  
with a cytoplasmic domain of APO4 and detecting a change in level of APO4  
activity. The method is performed in vivo or in vitro. APO polypeptides  
are all useful as immunogens for preparing antibodies. APO4 is also  
useful for diagnosis/treatment of developing antitubercles. APO4 is also  
abnormalities. APO8 was transfected to human breast carcinoma cell line  
MCF-7, and induced apoptosis.
```

XX	Human transmembrane activator CAML interactor protein; TACI; cytosstatic;
KW	cell proliferation; tumour; vulnerrary; renal cell cancer; mastocytoma;
KW	Kaposi's sarcoma; breast; ovarian carcinoma; rectal; throat; melanoma;
KW	colon; bladder; mammary adenocarcinoma; gastrointestinal; hyperplasia;
KW	pharyngeal squamous cell; stomach; cellular hyperproliferation; pannus;
KW	scleroderma; rheumatoid arthritis; scarring; mean survival time; liver;
KW	lung fibrosis; uterine; murine; a proliferation inducing ligand; mouse;
KW	APRIL; chimeric.
XX	
OS	Chimeric - Mus sp.
OS	Chimeric - Unidentified.
XX	
FH	Key
FT	Region
FT	Location/Qualifiers
FT	86..96
FT	/label= Myc_epitope
FT	97..104
FT	/label= Short_linker_region
FT	105..249
FT	/label= Extracellular_domain
FT	/note= "Extracellular domain of the murine APRIL coding
FT	sequence"
XX	
PN	WO200181417-A2.
XX	
PD	01-NOV-2001.
XX	
PF	27-APR-2001; 2001WO-US40626.
XX	
PR	27-APR-2000; 2000US-199946P.
XX	
PA	(BIOJ) BIOGEN INC.
PA	(APOT-) APOTECH R & D SA.
XX	
PI	Ambrose C, Thompson J, Schneider P, Rennert P;
DR	WPI; 2002-062027/08.
DR	N-PSDB; AAK98727.
XX	
PT	Treating mammal for condition associated with undesired cell
PT	proliferation e.g., solid tumour or reducing solid tumour size located in
PT	mammal comprises administering transmembrane activator CAML interactor
PT	protein reagent -
XX	
PS	Examples; Fig 6; 42pp; English.
XX	
CC	This sequence represents the protein of a myc-tagged murine APRIL (A
CC	Proliferation Inducing Ligand) construct. The invention relates to
CC	treating a mammal for a condition associated with undesired cell
CC	proliferation (e.g. a solid tumour, or reducing the size of a solid
CC	tumour located on or in a mammal) comprising administering a
CC	transmembrane activator CAML interactor protein (TACI) reagent. The TACI
CC	reagent has cytosstatic and vulnerary activity. Treating a mammal (e.g.
CC	human, cow, horse, dog, mouse, rat or cat) for a condition associated
CC	with undesired cell proliferation (e.g. cancer such as renal cell cancer,
CC	Kaposi's sarcoma, breast cancer, sarcoma, ovarian carcinoma, rectal
CC	cancer, throat cancer, melanoma, colon cancer, bladder cancer,
CC	mastocytoma, lung cancer, mammary adenocarcinoma, pharyngeal squamous
CC	cell carcinoma, gastrointestinal cancer or stomach cancer). The method is
CC	also useful for treating cellular hyperproliferation (hyperplasia) such
CC	as scleroderma, pannus formation in rheumatoid arthritis, post-surgical
CC	scarring and lung, liver and uterine fibrosis. The TACI reagent of the
CC	invention can extend mean survival time of a mammal by 25% as compared to
CC	the mean survival time of a mammal in the absence of administering the
CC	TACI reagent. The TACI reagent also reduces the size of the tumour by 25%
CC	or more.
XX	
XX	
Sequence	249 AA;
Query Match	8.4%; Score 21; DB 23; Length 249;
Best Local Similarity	100.0%; Pred. No. 5.1e-12;
Matches	21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
204	PDRAYNSCYSGVFHLLHOGDI 224

DB 203 PDRAVNSCYSAGVFHLHGDI 223

RESULT 55
 AAB62328
 ID AAB62328 standard; peptide; 15 AA.
 XX
 AC AAB62328;
 DT 29-JUN-2001 (first entry)
 XX
 DE Human TRDL-1gamma peptide epitope (residues 121-135).
 XX
 KW Tumour necrosis factor related death ligand-1gamma; TRDL-1gamma; TRDL;
 cell death; apoptosis; human; epitope.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 WO200125256-A2.
 PD 12-APR-2001.
 XX
 PF 06-OCT-2000; 2000WO-US27868.
 XX
 PR 06-OCT-1999; 99US-0157913.
 XX
 PA (UTAH) UNIV UTAH RES FOUND.
 XX
 PI Jones D, Manos E;
 XX
 DR WPI; 2001-281728/29.
 XX
 PT Isolated and purified polynucleotide encoding human tumor necrosis
 factor related death ligand (TRDL)-1 gamma useful for identifying
 PT agents that inhibit or enhance TRDL-1 gamma mediated induction of
 PT apoptosis -
 XX
 PS Example 6; Page 15; 39pp; English.
 XX
 CC The invention provides a human tumour necrosis factor related death
 CC ligand-1gamma (TRDL-1gamma). The TRDL-1gamma polypeptide can be
 CC expressed by standard recombinant methodology. TRDL-1gamma stimulates
 CC Jurkat cell death. It is useful for identifying agents capable of
 CC inhibiting or enhancing TRDL-1gamma mediated induction of apoptosis.
 CC The present sequence represents a TRDL-1gamma peptide epitope, used for
 CC generating rabbit polyclonal antibodies.
 CC
 Sequence 15 AA;
 Query Match 5.6%; Score 14; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.8e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 122 PINATSKDSDVTE 135
 Db 2 PINATSKDSDVTE 15
 RESULT 56
 AAG07407
 ID AAG07407 standard; Protein; 184 AA.
 XX
 AC AAG07407;
 XX
 DT 17-OCT-2000 (first entry)
 XX
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 4549.
 XX
 KW Protein identification; signal transduction pathway; metabolic pathway;
 hybridisation assay; genetic mapping; gene expression control; promoter;
 termination sequence.

XX Arabidopsis thaliana.
 OS
 PN EP1033405-A2.
 XX
 PD 06-SEP-2000.
 XX
 PF 25-FEB-2000; 2000EP-0301439.
 XX
 PR 25-FEB-1999; 99US-0121825.
 PR 05-MAR-1999; 99US-0123180.
 PR 09-MAR-1999; 99US-0123548.
 PR 23-MAR-1999; 99US-0125788.
 PR 25-MAR-1999; 99US-0126264.
 PR 29-MAR-1999; 99US-0126785.
 PR 01-APR-1999; 99US-0127462.
 PR 06-APR-1999; 99US-0128234.
 PR 08-APR-1999; 99US-0128714.
 PR 16-APR-1999; 99US-0129845.
 PR 19-APR-1999; 99US-0130077.
 PR 21-APR-1999; 99US-0130449.
 PR 23-APR-1999; 99US-0130510.
 PR 23-APR-1999; 99US-0130891.
 PR 28-APR-1999; 99US-0131449.
 PR 30-APR-1999; 99US-0132048.
 PR 30-APR-1999; 99US-0132407.
 PR 04-MAY-1999; 99US-0132484.
 PR 05-MAY-1999; 99US-0132485.
 PR 06-MAY-1999; 99US-0132486.
 PR 06-MAY-1999; 99US-0132487.
 PR 07-MAY-1999; 99US-0132863.
 PR 11-MAY-1999; 99US-0134256.
 PR 14-MAY-1999; 99US-0134218.
 PR 14-MAY-1999; 99US-0134219.
 PR 14-MAY-1999; 99US-0134221.
 PR 14-MAY-1999; 99US-0134370.
 PR 18-MAY-1999; 99US-0134768.
 PR 19-MAY-1999; 99US-0134941.
 PR 20-MAY-1999; 99US-0135124.
 PR 21-MAY-1999; 99US-0135353.
 PR 24-MAY-1999; 99US-0135629.
 PR 25-MAY-1999; 99US-0136021.
 PR 27-MAY-1999; 99US-0136392.
 PR 28-MAY-1999; 99US-0136782.
 PR 01-JUN-1999; 99US-0137222.
 PR 03-JUN-1999; 99US-0137528.
 PR 04-JUN-1999; 99US-0137502.
 PR 07-JUN-1999; 99US-0137724.
 PR 08-JUN-1999; 99US-0138094.
 PR 10-JUN-1999; 99US-0138540.
 PR 10-JUN-1999; 99US-0138847.
 PR 14-JUN-1999; 99US-0139119.
 PR 16-JUN-1999; 99US-0139452.
 PR 16-JUN-1999; 99US-0139453.
 PR 17-JUN-1999; 99US-0139492.
 PR 18-JUN-1999; 99US-0139454.
 PR 18-JUN-1999; 99US-0139455.
 PR 18-JUN-1999; 99US-0139456.
 PR 18-JUN-1999; 99US-0139457.
 PR 18-JUN-1999; 99US-0139458.
 PR 18-JUN-1999; 99US-0139459.
 PR 18-JUN-1999; 99US-0139460.
 PR 18-JUN-1999; 99US-0139461.
 PR 18-JUN-1999; 99US-0139462.
 PR 18-JUN-1999; 99US-0139463.
 PR 18-JUN-1999; 99US-0139750.
 PR 18-JUN-1999; 99US-0139763.
 PR 21-JUN-1999; 99US-0139817.
 PR 22-JUN-1999; 99US-0139899.
 PR 23-JUN-1999; 99US-0140353.
 PR 23-JUN-1999; 99US-0140354.
 PR 24-JUN-1999; 99US-0140695.
 PR 28-JUN-1999; 99US-0140823.

PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145324.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.

PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 3.2%; Score 8; DB 21; Length 184;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 GAALGAVA 43
Db 25 GAALGAVA 32

RESULT 57
AAG07406
ID AAG07406 standard; Protein; 223 AA.
XX AAG07406;
XX AC AAG07406;
XX DT 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 4548.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX XX

[illegible]

PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 3.2%; Score 8; DB 21; Length 223;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 36 GAALGAVA 43
Db 64 GAALGAVA 71

RESULT 58
AAU90178 standard; Peptide; 20 AA.

AC AAU90178;
DT 18-JUN-2002 (first entry)
XX Insulin/insulin-like growth factor receptor-binding peptide #2134.
DE
XX Cytostatic; antidiabetic; neuroprotective; cerebroprotective;
KM ophthalmological; insulin; receptor; gene therapy; diabetes;
KM insulin-like growth factor-1; IGF-1; tumour; prostate; breast;
KM diabetic retinopathy; neurological diseases; stroke;
KM diabetic neuropathy.

OS Synthetic.
XX WO200172771-A2.
XX 04-OCT-2001.
XX 29-MAR-2000; 2000WO-US08528.
XX 29-MAR-2000; 2000WO-US08528.
XX (DGIB-) DGI BIOTECHNOLOGIES LLC.

PA (NOVO) NOVO NORDISK AS.
XX Beasley J, Blume AJ, Schaeffer L, Pillutla R, Brandt J;
PI Brissette R, Spetzler J, Cheng W, Ostergaard S, Mandeckl WS;
PI Hansen PH, Ravera M, Hsiao K;
XX WPI; 2002-025774/03.
XX Modulating insulin activity in mammalian cells, for treating e.g.
PT diabetes and tumours, comprises using peptides that bind to insulin or
PT insulin-like growth factor receptors
XX Disclosure; Figure 4C; 390pp; English.
XX The invention relates to a method of modulating insulin activity in
CC mammalian cells by administering a peptide that binds the insulin
CC receptor (IR). A composition containing a peptide, optionally expressed
CC from gene therapy vectors, that binds to Site 1 of IR and an insulin
CC agonist are useful for treating diabetes. Also, peptides that are
CC antagonists of the insulin-like growth factor (IGF)-1 receptor are
CC useful for treating insulin-like growth factor-1 (IGF-1) receptor are
CC (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1
CC receptor agonists are useful for treating neurological diseases,
CC including stroke and diabetic neuropathy. The peptides are also useful in
CC screening for compounds that bind to IR or IGF-1 receptor, potential
CC therapeutics and research reagents. AAU88034-AAU90957 represent IR
CC and/or IGF-1 receptor-binding peptides and related amino acid sequences
XX of the invention.
XX Sequence 20 AA;

Query Match 2.8%; Score 7; DB 23; Length 20;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 33 LSWGAL 39
Db 8 LSWGAL 14

RESULT 59
AAU90722 standard; Peptide; 20 AA.

AC AAU90722;
DT 18-JUN-2002 (first entry)
XX Insulin/insulin-like growth factor receptor-binding peptide #2678.
DE
XX Cytostatic; antidiabetic; neuroprotective; cerebroprotective;
KM ophthalmological; insulin; receptor; gene therapy; diabetes;
KM insulin-like growth factor-1; IGF-1; tumour; prostate; breast;
KM diabetic retinopathy; neurological diseases; stroke;
KM diabetic neuropathy.

OS Synthetic.
XX WO200172771-A2.
XX 04-OCT-2001.
XX 29-MAR-2000; 2000WO-US08528.
XX 29-MAR-2000; 2000WO-US08528.
XX 29-MAR-2000; 2000WO-US08528.
XX (DGIB-) DGI BIOTECHNOLOGIES LLC.
XX (NOVO) NOVO NORDISK AS.
PI Beasley J, Blume AJ, Schaeffer L, Pillutla R, Brandt J;
PI Brissette R, Spetzler J, Cheng W, Ostergaard S, Mandeckl WS;
PI Hansen PH, Ravera M, Hsiao K;

DR WPI; 2002-025774/03.
XX
PT Modulating insulin activity in mammalian cells, for treating e.g.
PT diabetes and tumours, comprises using peptides that bind to insulin or
PT insulin-like growth factor receptors -
XX
PS Disclosure, Figure 11B; 390pp; English.
XX
CC The invention relates to a method of modulating insulin activity in
CC mammalian cells by administering a peptide that binds the insulin
CC receptor (IR). A composition containing a peptide, optionally expressed
CC from gene therapy vectors, that binds to site 1 of IR and an insulin
CC agonist are useful for treating diabetes. Also, peptides that are
CC antagonists of the insulin-like growth factor-1 (IGF-1) receptor are
CC useful for treating insulin-like growth factor (IGF)-sensitive tumours
CC (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1
CC receptor agonists are useful for treating neurological diseases,
CC including stroke and diabetic neuropathy. The peptides are also useful in
CC screening for compounds that bind to IR or IGF-1 receptor, potential
CC therapeutics and research reagents. AAU88034-AAU90957 represent IR
CC and/or IGF-1 receptor-binding peptides and related amino acid sequences
XX of the invention.

SO Sequence 20 AA;

Query Match 2.8%; Score 7; DB 23; Length 20;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 33 LSWGAL 39
|||
Db 8 LSWGAL 14

RESULT 60

AAB18725
ID AAB18725 standard; Protein; 27 AA.

AC AAB18725;

DT 22-JAN-2001 (first entry)

DE Amino acid sequence of mature protein dermaseptin b.

XX Dermaseptin; antibacterial; fungal growth; temporin; transgenic plant;
KW cationic peptide; pathogen resistance.

OS Phyllomedusa bicolor.

WO200055337-A1.

PD 21-SEP-2000.

PF 16-MAR-2000; 2000WO-CA00288.

PR 17-MAR-1999; 99US-0125072.

PA (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.

PI Misra S, Kay WD;

WPI; 2000-647077/62.

PT Transgenic plants resistant to broad spectrum of pathogens useful for
PT producing biologically active cationic peptides, comprises nucleic acid
PT molecule encoding temporin and/or dermaseptin peptides -

PS Claim 3; Page 47; 58pp; English.

CC AAB18725-36 represent mature processed forms of dermaseptin. Dermaseptin
CC has antibacterial activity, and inhibits fungal growth. Cationic
CC peptides derived from temporins and dermaseptins are used to produce
CC transgenic plants. The transgenic plants are useful for producing

CC biologically active cationic peptides such as temporins and dermaseptins
CC in large quantities. The peptide confers broad spectrum pathogen
CC resistance including enhanced resistance to both fungal and bacterial
CC pathogens in the transgenic plants. The transgenic plants may be used
CC in conventional agricultural applications such as food crops, medical
CC and other applications.

SO Sequence 27 AA;

Query Match 2.8%; Score 7; DB 21; Length 27;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 37 AALGAVA 43
|||
Db 16 AALGAVA 22

RESULT 61

AAB18726
ID AAB18726 standard; Protein; 31 AA.

AC AAB18726;

DT 22-JAN-2001 (first entry)

DE Amino acid sequence of mature protein dermaseptin B.

XX Dermaseptin; antibacterial; fungal growth; temporin; transgenic plant;
KW cationic peptide; pathogen resistance.

OS Phyllomedusa bicolor.

WO200055337-A1.

PD 21-SEP-2000.

PF 16-MAR-2000; 2000WO-CA00288.

PR 17-MAR-1999; 99US-0125072.

PA (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.

PI Misra S, Kay WD;

WPI; 2000-647077/62.

PT Transgenic plants resistant to broad spectrum of pathogens useful for
PT producing biologically active cationic peptides, comprises nucleic acid
PT molecule encoding temporin and/or dermaseptin peptides -

PS Claim 3; Page 47; 58pp; English.

CC AAB18725-36 represent mature processed forms of dermaseptin. Dermaseptin
CC has antibacterial activity, and inhibits fungal growth. Cationic
CC peptides derived from temporins and dermaseptins are used to produce
CC transgenic plants. The transgenic plants are useful for producing
CC biologically active cationic peptides such as temporins and dermaseptins
CC in large quantities. The peptide confers broad spectrum pathogen
CC resistance including enhanced resistance to both fungal and bacterial
CC pathogens in the transgenic plants. The transgenic plants may be used
CC in conventional agricultural applications such as food crops, medical
CC and other applications.

SO Sequence 31 AA;

Query Match 2.8%; Score 7; DB 21; Length 31;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 37 AALGAVA 43
|||
Db 20 AALGAVA 26

```
RESULT 62
AAB12436
ID AAB12436 standard; peptide; 31 AA.
XX
AC AAB12436;
XX
DT 20-OCT-2000 (first entry)
XX
DE Dermaseptin B amino acid sequence.
XX
KM CEMA; Pro-CEMA; dermaseptin B; temporin A; cecropin A; melittin;
KM CEMA 35S promoter; cationic polypeptide; antimicrobe; transgenic plant;
KM expression vector; agrobacillus; callus; phytopathogen; bacteria;
KM fungus; calli; antifungal; antibacterial.
XX
OS Unidentified.
XX
ID CN1249310-A.
XX
PD 05-APR-2000.
XX
PF 28-SEP-1998; 98CN-0112269.
XX
PR 28-SEP-1998; 98CN-0112269.
XX
PA (ZHOU/) ZHOU G.
XX
PI Zhou G;
XX
DR WPI; 2000-400710/35.
XX
PT Cationic polypeptide process for expressing antimicrobe in plant -
PS Claim 2; Page 1; 7pp; Chinese.
XX
CC The present invention describes a transgenic plant expression vector
CC containing three antimicrobe cationic polypeptides. The plant tissue is
CC introduced to these genes via agrobacillus and in the callus culture,
CC the callus resisting phytopathogen (bacteria and fungus) can be
CC externally chosen. Choosing these calli can regenerate plants and
CC directly test its antifungal and antibacterial powder. After these
CC transgenic plants are ripened, whole or partial plant can be harvested.
CC The present sequence represents a specifically claimed peptide from
CC the present invention.
XX
XX Sequence 31 AA;
XX
Query Match 2.8%; Score 7; DB 21; Length 31;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 37 AALGAVA 43
Db 20 AALGAVA 26
RESULT 63
AAB18748
ID AAB18748 standard; Protein; 32 AA.
XX
AC AAB18748;
XX
DT 22-JAN-2001 (first entry)
XX
DE A mature dermaseptin protein with a N-terminal extension.
XX
KM Dermaseptin; antibacterial; fungal growth; temporin; transgenic plant;
KM cationic peptide; pathogen resistance.
XX
OS Synthetic.
OS Phylomedusa bicolor.
```

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XX
PN WO200055337-A1.
XX
PD 21-SEP-2000.
XX
PF 16-MAR-2000; 2000WO-CA00288.
XX
PR 17-MAR-1999; 99US-0125072.
XX
PA (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.
XX
PI Misra S, Kay WD;
XX
DR WPI; 2000-647077/62.
DR N-PSDB; AAA75751.
XX
PT Transgenic plants resistant to broad spectrum of pathogens useful for
PT producing biologically active cationic peptides, comprises nucleic acid
PT molecule encoding temporin and/or dermaseptin peptides -
XX
PS Example; Page 51; 58pp; English.
XX
CC The present sequence represents a mature dermaseptin polypeptide
CC which has a N-terminal extension. Dermaseptin has antibacterial
CC activity, and inhibits fungal growth. Cationic peptides derived from
CC temporins and dermaseptins are used to produce transgenic plants. The
CC transgenic plants are useful for producing biologically active cationic
CC peptides such as temporins and dermaseptins in large quantities. The
CC peptide confers broad spectrum pathogen resistance including enhanced
CC resistance to both fungal and bacterial pathogens in the transgenic
CC plants. The transgenic plants may be used in conventional agricultural
CC applications such as food crops, medical and other applications.
XX
SQ Sequence 32 AA;
XX
Query Match 2.8%; Score 7; DB 21; Length 32;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 37 AALGAVA 43
Db 21 AALGAVA 27
RESULT 64
AAW34538
ID AAW34538 standard; peptide; 45 AA.
XX
AC AAW34538;
XX
DT 26-MAR-1998 (first entry)
XX
DE Lipase signal peptide.
XX
KW Promoter; lipase gene; Burkholderia genus microbe; lipase production.
XX
OS Pseudomonas cepacia.
XX
PN JP09322776-A.
XX
PD 16-DEC-1997.
XX
PF 31-MAY-1996; 96JP-0160637.
XX
PR 31-MAY-1996; 96JP-0160637.
XX
PA (CHCC ) CHISSO CORP.
XX
DR WPI; 1998-094675/09.
DR N-PSDB; AAT99136.
XX
PT Recombinant plasmid used to prepare lipase - using host-vector
PT system for Burkholderia genus microbe
```

XX PS Claim 6; Page 8; 12pp; Japanese.
XX CC This sequence represents the lipase signal peptide. The lipase gene
CC promoter region can be used in the plasmid in which the invention. The plasmid
CC of the invention is a recombinant plasmid in which a DNA fragment
CC containing the promoter region of the lipase gene (comprising a sequence
CC encoding a signal peptide) and a gene controlling lipase activity
CC expression is recombinated to a broad host vector. The plasmid can be used
CC to transform a Burkholderia genus microbe, which is then cultured to
CC produce a recombinant lipase. The recombinant lipase can be prepared in
CC large amounts.
SQ Sequence 45 AA;

Query Match 2.8%; Score 7; DB 19; Length 45;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

40 GAVACAM 46
12 GAVACAM 18

RESULT 65
AAM86507
ID AAM86507 standard; Protein; 61 AA.
XX AC AAM86507;
XX DT 07-NOV-2001 (first entry)
XX DE Human immune/haematopoietic antigen SEQ ID NO:14100.
XX KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX KW cytostatic; gene therapy; vaccine; metastasis.
XX OS Homo sapiens.
XX PN WO200157182-A2.
XX PD 09-AUG-2001.
XX PF 17-JAN-2001; 2001WO-US01354.
XX PR 31-JAN-2000; 2000US-0179065.
XX PR 04-FEB-2000; 2000US-0180628.
XX PR 24-FEB-2000; 2000US-0184664.
XX PR 02-MAR-2000; 2000US-0186350.
XX PR 16-MAR-2000; 2000US-0189874.
XX PR 17-MAR-2000; 2000US-0190076.
XX PR 18-APR-2000; 2000US-0198123.
XX PR 19-MAY-2000; 2000US-0205515.
XX PR 07-JUN-2000; 2000US-0209467.
XX PR 28-JUN-2000; 2000US-0214886.
XX PR 30-JUN-2000; 2000US-0215135.
XX PR 07-JUL-2000; 2000US-0216647.
XX PR 07-JUL-2000; 2000US-0216880.
XX PR 11-JUL-2000; 2000US-0217487.
XX PR 11-JUL-2000; 2000US-0217496.
XX PR 14-JUL-2000; 2000US-0218290.
XX PR 26-JUL-2000; 2000US-0220963.
XX PR 14-AUG-2000; 2000US-0224518.
XX PR 14-AUG-2000; 2000US-0224519.
XX PR 14-AUG-2000; 2000US-0225213.
XX PR 14-AUG-2000; 2000US-0225214.
XX PR 14-AUG-2000; 2000US-0225266.
XX PR 14-AUG-2000; 2000US-0225267.
XX PR 14-AUG-2000; 2000US-0225268.
XX PR 14-AUG-2000; 2000US-0225270.
XX PR 14-AUG-2000; 2000US-0225447.
XX PR 14-AUG-2000; 2000US-0225757.

PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 08-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.

PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-483426/52.
DR N-PSDB; AAK59288.
XX
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
Claim 11; SEQ ID NO 14100; 3071pp + Sequence Listing; English.
CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 61 AA;

Query Match 2.8%; Score 7; DB 22; Length 61;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 97 GERSRKR 103
Db 6 GERSRKR 12
RESULT 66
AAB16374
ID AAB16374 standard; Protein; 62 AA.
XX
AC AAB16374;
XX
DT 24-OCT-2000 (first entry)
XX
DE Eucalyptus grandis diphenol oxidase protein sequence SEQ ID NO:300.
XX
KW Plant; lignin; lignin biosynthetic pathway; Eucalyptus grandis;
KM Pinus radiata; Monterey pine.
XX
OS Eucalyptus grandis.
XX
PN WO200022099-A1.
XX
PD 20-APR-2000.
XX
PF 06-OCT-1999; 99WO-NZ00168.
XX
PR 09-OCT-1998; 98US-0169789.
PR 14-JUL-1999; 99US-0143811.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
XX
PI Bloksberg LN, Havukkala IJ;
XX
DR WPI; 2000-317962/27.
XX
PT Novel polynucleotide encoding enzymes involved in lignin-biosynthetic
PT pathway useful for producing transgenic plants especially eucalyptus
PT and pine species having altered lignin content, composition and
PT structure -
XX
XX
PS Claim 18; Page 156; 213pp; English.
XX
CC The present invention describes isolated polynucleotides and proteins
CC encoding and representing the enzymes cinnamate 4-hydroxylase (C4H),
CC coumarate 3-hydroxylase (C3H), phenolase (PNL), O-methyl transferase
CC (OMT), cinnamyl alcohol dehydrogenase (CAD), cinnamoyl-CoA reductase
CC (CCR), phenylalanine ammonia-lyase (PAL), 4-coumarate:CoA ligase (4CL),
CC coniferol glucosyl transferase (CGT), coniferin beta-glucosidase (CBG),
CC laccase, peroxidase, ferulate-5-hydroxylase (F5H), alpha-amylase,
CC caffeic acid methyl transferase, caffeoyl CoA methyl transferase,
CC coumarate CoA ligase, cytochrome P450 LXXIA, diphenol oxidase, flavanol
CC glucosyl transferase, flavonoid hydroxylase, and isoflavone reductase,
CC which are involved in the lignin biosynthetic pathway. The
CC polynucleotides can be used for modulating lignin content, lignin
CC composition and the structure of a plant, especially eucalyptus and pine
CC species, and for modifying the activity of an enzyme involved in lignin
CC biosynthetic pathway, and for producing a plant having altered lignin
CC content, composition and structure. They can be used for designing probes
CC and primers useful for detecting similar DNA and RNA sequences in any
CC organism and for PCR amplification. The lignin content can be efficiently
CC modified using the polynucleotides. AAK67908 to AAK68201 and AAB16341 to
CC AAB16449 represent polynucleotide and protein sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 62 AA;

Query Match 2.8%; Score 7; DB 21; Length 62;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 242 GTFLGFV 248
|||||||

Db 5 GTFTGFV 11

RESULT 67

ID ABG12905 standard; Protein; 65 AA.

AC ABG12905;

DT 13-FEB-2002 (first entry)

DE Novel human diagnostic protein #12896.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN WO200175067-A2.

PF 11-OCT-2001.

PR 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI; 2001-639362/73.

DR N-PSDB; AAS77092.

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -

PS Claim 20; SEQ ID No 43264; 103bp; English.

CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

SO Sequence 65 AA;

Query Match 2.8%; Score 7; DB 22; Length 65;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 56 QSLRREV 62
Db 39 QSLRREV 45

RESULT 68

ID AAM84103 standard; Protein; 73 AA.

AC AAM84103;

DT 07-NOV-2001 (first entry)

DE Human immune/haematopoietic antigen SEQ ID NO:11696.

KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis.

OS Homo sapiens.

PN WO200157182-A2.

PD 09-AUG-2001.

PF 17-JAN-2001; 2001WO-US01354.

PR 31-JAN-2000; 2000US-0179065.

PR 04-FEB-2000; 2000US-0180628.

PR 24-FEB-2000; 2000US-0184664.

PR 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0189874.

PR 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.

PR 19-MAY-2000; 2000US-0205515.

PR 07-JUN-2000; 2000US-0209467.

PR 28-JUN-2000; 2000US-0214886.

PR 30-JUN-2000; 2000US-0215135.

PR 07-JUL-2000; 2000US-0216647.

PR 07-JUL-2000; 2000US-0216880.

PR 11-JUL-2000; 2000US-0217487.

PR 11-JUL-2000; 2000US-0217496.

PR 14-JUL-2000; 2000US-0218290.

PR 26-JUL-2000; 2000US-0220963.

PR 26-JUL-2000; 2000US-0220964.

PR 14-AUG-2000; 2000US-0224518.

PR 14-AUG-2000; 2000US-0224519.

PR 14-AUG-2000; 2000US-0225213.

PR 14-AUG-2000; 2000US-0225214.

PR 14-AUG-2000; 2000US-0225266.

PR 14-AUG-2000; 2000US-0225267.

PR 14-AUG-2000; 2000US-0225268.

PR 14-AUG-2000; 2000US-0225447.

PR 14-AUG-2000; 2000US-0225477.

PR 14-AUG-2000; 2000US-0225757.

PR 14-AUG-2000; 2000US-0225758.

PR 14-AUG-2000; 2000US-0225759.

PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 01-DEC-2000; 2000US-0250160.
PR

PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-483426/52.
DR N-PSDB; AAK56884.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
PT
XX
PS Claim 11; SEQ ID NO 11696; 3071pp + Sequence Listing; English.
XX
CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytosstatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 73 AA;
Query Match 2.8%; Score 7; DB 22; Length 73;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 141 ALRRGRG 147
Db 65 ALRRGRG 71
RESULT 69
AAB18724
ID AAB18724 standard; Protein; 78 AA.
XX
AC AAB18724;
XX
DT 22-JAN-2001 (first entry)
XX
DE A dermaseptin precursor polypeptide.
XX
KW Dermaseptin; antibacterial; fungal growth; temporin; transgenic plant;
KW cationic peptide; pathogen resistance.
XX
OS Phyllomedusa bicolor.
XX
PN WO200055337-A1.
XX
PD 21-SEP-2000.

XX 16-MAR-2000; 2000WO-CA00288.
PF
XX
PR 17-MAR-1999; 99US-0125072.
XX
PA (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.
XX
PI Misra S, Kay WD;
XX
DR WPI; 2000-647077/62.
DR N-PSDB; AAA75749.
XX
PT Transgenic plants resistant to broad spectrum of pathogens useful for
PT producing biologically active cationic peptides, comprises nucleic acid
PT molecule encoding temporin and/or dermaseptin peptides -
XX
PS Disclosure; Page 47; 58pp; English.
XX
CC The present sequence represents a dermaseptin precursor polypeptide.
CC The precursor is processed to produce two mature forms, dermaseptin b
CC (AAB18725) and dermaseptin B (AAB18726). Dermaseptin has antibacterial
CC activity, and inhibits fungal growth. Cationic peptides derived from
CC transgenic plants are useful for producing biologically active cationic
CC peptides such as temporins and dermaseptins in large quantities. The
CC transgenic plants are useful for producing biologically active cationic
CC peptides such as temporins and dermaseptins in large quantities. The
CC peptide confers broad spectrum pathogen resistance including enhanced
CC resistance to both fungal and bacterial pathogens in the transgenic
CC plants. The transgenic plants may be used in conventional agricultural
CC applications such as food crops, medical and other applications.
XX
SQ Sequence 78 AA;
Query Match 2.8%; Score 7; DB 21; Length 78;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 37 AALGAVV 43
Db 64 AALGAVV 70
RESULT 70
AAB64816
ID AAB64816 standard; Protein; 79 AA.
XX
AC AAB64816;
XX
23-MAR-2001 (first entry)
XX
Human secreted protein sequence encoded by gene 44 SEQ ID NO:102.
XX
KW Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic;
KW antiproliferative; cyostatic; cardiant; vasotropic; cerebroprotective;
KW neurotropic; neuroprotective; antibacterial; virucide; fungicide;
KW ophthalmological; autoimmune disease; hyperproliferative disorder;
KW cardiovascular disorder; cerebrovascular disorder; infection; chemotaxis;
KW nervous system disorder; ocular disorder; skin aging; wound healing;
KW food additive; tissue regeneration.
XX
OS Homo sapiens.
XX
PN WO200077256-A1.
XX
PD 21-DEC-2000.
XX
PF 01-JUN-2000; 2000WO-US14963.
XX
PR 11-JUN-1999; 99US-0138631.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Komatsoulis GA;
XX

DR WPI; 2001-032315/04.
DR N-PSDB; AAF33138.
XX
PT Isolated nucleic acid molecule encoding a human secreted protein is
PT used in preventing, treating or ameliorating a medical condition -
XX
PS Claim 11; Page 472; 506pp; English.
XX
CC Polynucleotide sequences AAF33095 - AAF33142 encode human secreted
CC proteins AAB64773 - AAB64820. Fragments of the secreted proteins and
CC amino acid sequences which share homology with the fragments are
CC represented in AAB64821 - AAB64880. The genes and proteins have
CC activities dependent on the tissues and cells in which they are
CC expressed. Examples of their activities and the activities of their
CC agonists and antagonists include, immunosuppressive; antiarthritic;
CC antirheumatic; antiproliferative; cyostatic; cardiant; vasotropic;
CC cerebroprotective; neurotropic; neuroprotective; antibacterial; virucide;
CC fungicide; and ophthalmological. The secreted proteins, polynucleotides,
CC antagonists and agonists may be useful in treating, preventing and
CC diagnosing diseases and disorders such as autoimmune diseases e.g.
CC rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the
CC breast or liver, cardiovascular disorders e.g. cardiac arrest,
CC cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous
CC system disorders e.g. Alzheimer's disease, infections caused by bacteria,
CC viruses and fungi and ocular disorders e.g. corneal infection. The
CC polypeptides can also be used to aid wound healing and epithelial cell
CC proliferation, to prevent skin aging due to sunburn, to maintain organs
CC before transplantation, for supporting cell culture of primary tissues,
CC to regenerate tissues and in chemotaxis. The polypeptides can also be
CC used as a food additive or preservative to increase or decrease storage
CC capabilities. Included in the invention are sequences AAB64772 and
CC AAF33095 - AAF33142 which are used in the isolation and characterisation
CC of the nucleotide and protein sequences of the invention.
XX
SQ Sequence 79 AA;
Query Match 2.8%; Score 7; DB 22; Length 79;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 209 NSCYSAG 215
Db 36 NSCYSAG 42
RESULT 71
AAM89786
ID AAM89786 standard; Protein; 83 AA.
XX
AC AAM89786;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen SEQ ID NO:17379.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cyostatic; gene therapy; vaccine; metastasis.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
XX

PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.

PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPT; 2001-483426/52.
DR N-PSDB; AAK62567.
XX
XX
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
XX
PS Claim 11; SEQ ID NO 17379; 3071bp + Sequence Listing; English.
XX
CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)

CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 83 AA;

Query Match 2.8%; Score 7; DB 22; Length 83;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

5 SPFLAP 11
11 SPFLAP 17

RESULT 72

AAU44493
ID AAU44493 standard; Protein; 87 AA.

AC AAU44493;

DT 27-FEB-2002 (first entry)

DE Propionibacterium acnes immunogenic protein #5389.

XX
KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.

XX OS Propionibacterium acnes.

XX PN WO200181581-A2.

XX PD 01-NOV-2001.

XX PF 20-APR-2001; 2001WO-US12865.

XX PN 21-APR-2000; 2000US-199047P.

XX PR 02-JUN-2000; 2000US-208841P.

XX PR 07-JUL-2000; 2000US-216747P.

XX PA (CORI-) CORIXA CORP.

XX PI Skelky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;

XX PI L'maisonneuve J, Zhang Y, Jen S, Carter D;

XX DR WPI; 2001-616774/71.

XX DR N-PSDB; AAS59522.

XX PT Propionibacterium acnes polypeptides and nucleic acids useful for
XX PT vaccinating against and diagnosing infections, especially useful for
XX PT treating acne vulgaris -

XX PS Example 1; SEQ ID No 5688; 1069pp; English.

XX
CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central

CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA).
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 87 AA;

Query Match 2.8%; Score 7; DB 22; Length 87;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 101 RKRRVL 107
27 RKRRVL 33

RESULT 73

AAW82267
ID AAW82267 standard; Protein; 96 AA.

AC AAW82267;

DT 18-FEB-1999 (first entry)

DE Human NTN-2 protein fragment.

XX
KW NTN-2; tumour necrosis factor; TNF; human; diagnosis; screening;
KW immunogen; gene therapy; modulator; biopharmaceutical industry;
KW cell growth; cell differentiation; cell function.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Protein 1..96 /label= NTN-2

XX FT /note= "Partial sequence, no start codon given"

XX FT Misc-difference 26 /label= unknown

XX PN WO9855620-A1.

XX PD 10-DEC-1998.

XX PF 03-JUN-1998; 98WO-US11153.

XX PR 21-NOV-1997; 97US-0066386.

XX PR 06-JUN-1997; 97US-0048776.

XX PA (REGG-) REGENERON PHARM INC.

XX PI Masiakowski P, Valenzuela D;

XX DR WPI; 1999-045793/04.

XX DR N-PSDB; AAV73306.

XX PT Newly isolated nucleotide encoding human NTN-2 - useful in methods
XX PT of diagnosis and in the treatment of the human or animal body
XX PS Example 1; Page 14; 26pp; English.

XX
CC This sequence represents a fragment of the human tumour necrosis factor
CC (TNF) homologue, NTN-2. This polypeptide and antibodies generated
CC from the polypeptide form compositions that are useful in diagnosis (e.g.

CC genetic hybridization screens for human NTN-2 transcripts), gene therapy
CC (to modulate human NTN-2 gene expression) and the biopharmaceutical
CC industry (e.g. reagents for screening chemical libraries for suitable
CC pharmaceutical agents). The polypeptides are also useful as immunogens,
CC targets in screening assays, and bioactive reagents for modulating cell
CC growth, differentiation and/or function. The nucleotides are useful as
CC translatable transcripts, hybridization probes, PCR primers, diagnostic
CC nucleotides, and as agents in detecting human NTN-2 genes/transcripts
CC (including variants).
XX
SQ Sequence 96 AA;

Query Match 2.8%; Score 7; DB 20; Length 96;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 209 NSCYSAG 215
Db 54 NSCYSAG 60

RESULT 74

AAW82269
ID AAW82269 standard; Protein; 96 AA.

AC AAW82269;

DT 18-FEB-1999 (first entry)

DE Human NTN-2 partial protein sequence.

XX NTN-2; tumour necrosis factor; TNF; human; diagnosis; screening;
KW immunogen; gene therapy; modulator; biopharmaceutical industry;
KW cell growth; cell differentiation; cell function.

OS Homo sapiens.

XX
FH Key Location/Qualifiers
FT Protein 1..96
FT /label= NTN-2
FT /note= "Partial sequence, no start codon given"

FT Misc-difference 26
FT /label= unknown
XX
PN WO9855621-A1.
XX 10-DEC-1998.

PD 03-JUN-1998; 98WO-US11294.
PR 21-NOV-1997; 97US-0066387.
PR 06-JUN-1997; 97US-0048776.

XX
PA (REGG-) REGENERON PHARM INC.
XX
PI Maslakowski P, Valenzuela D;
XX WPI: 1999-045794/04.
DR N-PSDB; AAV73308.

XX
PT Newly isolated nucleotide encoding human NTN-2 - useful in methods
PT of diagnosis and in the treatment of the human or animal body
XX
PS Example 1; Page 14; 26pp; English.

CC This sequence encodes a fragment of the human tumour necrosis factor
CC (TNF) homologue, NTN-2. This polypeptide and antibodies generated
CC from the polypeptide form compositions that are useful in diagnosis (e.g.
CC genetic hybridization screens for human NTN-2 transcripts), gene therapy
CC (to modulate human NTN-2 gene expression) and the biopharmaceutical
CC industry (e.g. reagents for screening chemical libraries for suitable
CC pharmaceutical agents). The polypeptides are also useful as immunogens,
CC targets in screening assays, and bioactive reagents for modulating cell

CC growth, differentiation and/or function. The nucleotides are useful as
CC translatable transcripts, hybridization probes, PCR primers, diagnostic
CC nucleotides, and as agents in detecting human NTN-2 genes/transcripts
CC (including variants).
XX
SQ Sequence 96 AA;

Query Match 2.8%; Score 7; DB 20; Length 96;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 209 NSCYSAG 215
Db 54 NSCYSAG 60

RESULT 75

AAO08276
ID AAO08276 standard; Protein; 105 AA.

AC AAO08276;

DT 06-NOV-2001 (first entry)

DE Human polypeptide SEQ ID NO 22168.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.

OS Homo sapiens.

XX
PN WO200164835-A2.

PD 07-SEP-2001.

PF 26-FEB-2001; 2001WO-US04927.

PR 28-FEB-2000; 2000US-0515126.

PR 18-MAY-2000; 2000US-0577409.

XX
PA (HYSE-) HYSEQ INC.

XX
PI Tang YT, Liu C, Drmanac RT;

XX
DR WPI: 2001-514838/56.
DR N-PSDB; AAI88207.

XX
PT Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders -
XX
PS Claim 20; SEQ ID NO 22168; 1399pp + Sequence Listing; English.

XX
CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity relating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 105 AA;

Query Match 2.8%; Score 7; DB 22; Length 105;

Best Local Similarity 100.0%; Pred. No. 96;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 LAPKGP 15
| | | | | | | |
Db 87 LAPKGP 93

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Job time : 40 secs

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 07:31:11 ; Search time 75 Seconds
(without alignments)
444.169 Million cell updates/sec

Title: US-09-724-341-8
Perfect score: 1304
Sequence: 1 MPASSPFLAPKGPNGMG.....RARAKNLSPHGTFLGFVKL 250

Scoring table: BLOSUM62
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Searched: 908470 seqs, 133250620 residues
a1 number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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22:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
23:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1304	100.0	250	20	AAV06485	Human tumour-asso
2	1304	100.0	250	20	AAV17832	Human PRO715 prote
3	1304	100.0	250	20	AAV04283	Human APRIL protei
4	1304	100.0	250	20	AAW88368	Tumour necrosis fa
5	1304	100.0	250	21	AAV933692	Amino acid sequenc
6	1304	100.0	250	21	AAE01323	Human PRO715 polyp
7	1304	100.0	250	22	AAE09243	Human APRIL protei
8	1304	100.0	250	22	AAE62329	Human TRDL-1alpha
9	1304	100.0	250	22	AAV71981	Human TNF and Apol
10	1304	100.0	250	23	AAU99305	Human tumour necro

11	1304	100.0	250	23	ABB81486	Human ZTNF2 amino
12	1304	100.0	250	23	ABP47228	Human Blys binding
13	1304	100.0	250	23	AAU79155	Human APRIL (a pro
14	1299	99.6	250	20	AAW93588	Human TNRL1-beta p
15	1299	99.6	250	21	AAV79670	Human death recept
16	1299	99.6	250	23	AAE15502	Human APRIL G70 pr
17	1299	99.6	260	20	AAV60542	Human normal bladd
18	1297	99.5	260	21	AAE54342	Human pancreatic c
19	1296	99.4	250	20	AAU05745	Tumour necrosis fa
20	1296	99.4	250	23	AAU99510	Human tumour necro
21	1296	99.4	250	23	AAU75406	Tumour necrosis fa
22	1290	98.9	248	23	AAE15482	Human APRIL G70 pr
23	1285	98.5	247	20	AAV28836	Human TNF-related
24	1285	98.5	247	22	AAE62327	Human TRDL-1gamma
25	1241	95.2	248	22	AAE07877	Human APRIL protei
26	1206	92.5	233	20	AAV09551	Human TRAILK-3 pr
27	1203	92.3	233	23	AAU99508	Human tumour necro
28	1203	92.3	233	22	AAU75402	Tumour necrosis fa
29	1200	92.0	234	22	AAE62330	Human TRDL-1beta p
30	1199	91.9	233	18	AAW37002	Human tumour necro
31	1195	91.6	234	20	AAV28835	Human TNF-related
32	1195	91.6	244	20	AAV74026	Human prostate tum
33	1187	91.0	234	23	AAU99511	Human tumour necro
34	1187	91.0	234	23	AAU75407	Tumour necrosis fa
35	1053	80.8	205	20	AAV22225	Human TNFL2 protei
36	1013.5	77.7	241	20	AAW93589	Mouse TNRL1-beta p
37	1006	77.1	240	23	AAE15483	Mouse APRIL/G70 pr
38	978.5	75.0	232	21	AAV79672	Mouse death recept
39	967.5	74.2	232	20	AAV04284	Mouse APRIL protei
40	967.5	74.2	232	22	AAE07878	Mouse APRIL protei
41	858	65.8	168	18	AAW37003	Human tumour necro
42	858	65.8	168	23	AAU99509	Human tumour necro
43	858	65.8	168	23	AAU75403	Tumour necrosis fa
44	762	58.4	147	20	AAW88369	Tumour necrosis fa
45	759	58.2	177	23	AAO14134	Protein of a FLAG

ALIGNMENTS

RESULT 1	AAV06485	
ID	AAV06485	standard; Protein; 250 AA.
XX		
AC	AAV06485;	
XX		
DT	27-SEP-1999	(first entry)
XX		
DE	Human tumour-associated protein PRO715.	
XX		
KW	PRO715; UNQ383; cancer; tumour necrosis family; diagnosis; therapy; human.	
KW	human.	
XX		
OS	Homo sapiens.	
XX		
PN	WO9935170-A2.	
XX		
PD	15-JUL-1999.	
XX		
PF	05-JAN-1999;	99WO-US00106.
XX		
PR	20-NOV-1998;	98US-0109304.
PR	05-JAN-1998;	98US-0070440.
PR	29-APR-1998;	98US-0083500.
PR	22-MAY-1998;	98US-0086414.
PR	10-JUN-1998;	98US-0088742.
PR	10-NOV-1998;	98US-0107783.
XX		
PA	(GETH) GENENTECH INC.	
XX		
PI	Botstein D, Goddard A, Gurney AL, Hillan KJ, Lawrence DA;	
PI	Roy MA, Wood WT;	
XX		

KW immune disorder; cancer.

XX Homo sapiens.

OS WO9912965-A2.

XX 18-MAR-1999.

XX 11-SEP-1998; 98WO-US19191.

XX 26-MAR-1998; 98US-0079384.

XX 12-SEP-1997; 97US-0058786.

XX (BIOJ) BIOGEN INC.

XX Techopp J;

XX WPI; 1999-215028/18.

XX N-PSDB; AAX30124.

PT A Proliferating Inducing Agent (APRIL), a member of the Tumour Necrosis Factor Family - useful as diagnostic agents and for prevention or treatment of immune disorders and cancer

PS Claim 12; Page 46; 47pp; English.

XX The present sequence represents a proliferating inducing agent (APRIL) isolated from human. APRIL is a member of the tumour necrosis factor family, and essentially free of normally associated proteins. APRIL and APRIL antibodies are useful in pharmaceutical compositions for preventing or reducing severity of an autoimmune disease or an immune response to tissue graft. The composition is also useful for stimulating or suppressing the immune system, and treating cancer. APRIL is also useful for treating APRIL-related disorders by delivering via a vector (preferably viral vector) (gene therapy) into a mammalian (preferably human) cell. Labeled APRIL and fragments are useful for identifying APRIL receptors by screening compositions. Antisense DNA and antibodies and modified APRIL (preferably an anti-APRIL receptor antibody) are useful as blocking agents for inducing cell death by interfering with APRIL receptors. The blocking agent is preferably administered with interferon- γ and treats, suppresses or alters an immune response involving a signalling pathway between APRIL and its receptor (preferably involving human carcinoma cells); and also treats, suppresses or alters the progression of cancer (preferably at least one chemotherapeutic agent is also administered, and radiation therapy is also given to the patient).

XX Sequence 250 AA;

Query Match 100.0%; Score 1304; DB 20; Length 250;

Best Local Similarity 100.0%; Pred. No. 4.1e-127;

Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MPASSPFLAPKPGPGNMGVPVREPALSVALWLSWGALGAVACAMALLTQOTELQSLRR 60

DB 1 MPASSPFLAPKPGPGNMGVPVREPALSVALWLSWGALGAVACAMALLTQOTELQSLRR 60

OY 61 EVSRLOGTGSPSONGEGYPMQSLPEQSSDALFAWENGERSRKRRAVLTKOKKHSHVLHL 120

DB 61 EVSRLOGTGSPSONGEGYPMQSLPEQSSDALFAWENGERSRKRRAVLTKOKKHSHVLHL 120

OY 121 VPINATSKDSDVTEVMQPALRRGRLQAQGYGVRIQDAGVLLYSQVLFQDVTFTMGQ 180

DB 121 VPINATSKDSDVTEVMQPALRRGRLQAQGYGVRIQDAGVLLYSQVLFQDVTFTMGQ 180

OY 181 VVSREGQGRQETLFRICIRSMPSHPDRAYNSCYAGVFHLHOGDILSVIIPRAKLNLS 240

DB 181 VVSREGQGRQETLFRICIRSMPSHPDRAYNSCYAGVFHLHOGDILSVIIPRAKLNLS 240

OY 241 HGTFLGFVKL 250

DB 241 HGTFLGFVKL 250

RESULT 4
AAW88368
ID AAW88368 standard; Protein; 250 AA.

XX AAW88368;

XX 26-APR-1999 (first entry)

XX Tumour necrosis factor-gamma.

XX Tumour necrosis factor-gamma; TNF-gamma; human; inflammation;

XX cancer; tumour; metastasis; graft versus host disease;

XX drug screening; therapy; diagnosis.

XX Homo sapiens.

XX WO9900518-A1.

XX 07-JAN-1999.

XX 12-JUN-1998; 98WO-US12101.

XX 26-JUN-1997; 97US-0883086.

XX (ABBO) ABBOTT LAB.

XX Wiley SR;

XX WPI; 1999-095761/08.

XX N-PSDB; AAX06771.

PT Tumour necrosis factor gamma detects target polynucleotides - useful for, e.g. treating inflammation, cancer and graft versus host disease

PS Claim 16; Page 84-85; 106pp; English.

XX This is the amino acid sequence of human tumour necrosis factor gamma (TNFG), a novel member of the TNF family of ligands. The invention provides a method of producing TNFG polypeptide using a recombinant expressing system comprising a nucleic acid sequence (see AAX06771) encoding TNFG and transformed host cells. Also provided are a procedure of producing biologically active soluble TNFG (see AAW88368), which can be used to treat deficiencies of TNFG and disease conditions ameliorated by TNFG. Antibodies, antagonists and inhibitors of such a polypeptide may be used to treat TNFG-associated diseases, tumours or metastases, and to screen for, diagnose and monitor conditions attributable to TNFG, especially inflammation, cancer and graft versus host disease. Cells expressing TNFG on their surface can be used to screen for (ant)agonists, and to detect receptor binding.

XX Sequence 250 AA;

Query Match 100.0%; Score 1304; DB 20; Length 250;

Best Local Similarity 100.0%; Pred. No. 4.1e-127;

Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MPASSPFLAPKPGPGNMGVPVREPALSVALWLSWGALGAVACAMALLTQOTELQSLRR 60

DB 1 MPASSPFLAPKPGPGNMGVPVREPALSVALWLSWGALGAVACAMALLTQOTELQSLRR 60

OY 61 EVSRLOGTGSPSONGEGYPMQSLPEQSSDALFAWENGERSRKRRAVLTKOKKHSHVLHL 120

DB 61 EVSRLOGTGSPSONGEGYPMQSLPEQSSDALFAWENGERSRKRRAVLTKOKKHSHVLHL 120

OY 121 VPINATSKDSDVTEVMQPALRRGRLQAQGYGVRIQDAGVLLYSQVLFQDVTFTMGQ 180

DB 121 VPINATSKDSDVTEVMQPALRRGRLQAQGYGVRIQDAGVLLYSQVLFQDVTFTMGQ 180

OY 181 VVSREGQGRQETLFRICIRSMPSHPDRAYNSCYAGVFHLHOGDILSVIIPRAKLNLS 240

Db 181 VVSREGQGRQETLFR CIRSMPSHPDRAYNSCYSAGVFHLHGDILSVIIPRARA KNLSP 240
QY 241 HGTFLGFVKL 250
Db 241 HGTFLGFVKL 250

RESULT 5
AA93692
ID AAY93692 standard; Protein; 250 AA.
AC AAY93692;
DT 03-OCT-2000 (first entry)
DE Amino acid sequence of novel polypeptide PRO715.
XX
KW PRO201; PRO292; PRO327; PRO1265; PRO344; PRO343; PRO347; PRO357;
KM PRO715; PRO1017; PRO1112; PRO509; PRO853; PRO882; tumour cell;
tumorigenesis; cancer; neoplastic cell growth; cell proliferation.
Homo sapiens.

Key Location/Qualifiers
FH Peptide 1..40
FT /note= "signal sequence"
FT Region 34..45
FT /note= "prokaryotic membrane lipoprotein attachment site"
FT Modified-site 36..42
FT /note= "N-myristoylation site"
FT Modified-site 40..46
FT /note= "N-myristoylation site"
FT Modified-site 124..128
FT /note= "N-glycosylation site"
FT Modified-site 156..164
FT /note= "tyrosine kinase phosphorylation site"
FT Modified-site 179..185
FT /note= "N-myristoylation site"
FT Modified-site 242..248
FT /note= "N-myristoylation site"

WO200037640-A2.
XX
PN 29-JUN-2000.
XX
PF 16-DEC-1999; 99WO-US30095.
XX
PR 22-DEC-1998; 98US-0113296.
PR 08-MAR-1999; 99WO-US05028.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 30-NOV-1999; 99WO-US28313.
PR 30-NOV-1999; 99WO-US28409.
PR 01-DEC-1999; 99WO-US28301.
PR 02-DEC-1999; 99WO-US28565.
XX
PA (GETH) GENENTECH INC.
XX
PI Botstein D, Goddard A, Gurney AL, Hillan K, Lawrence DA, Roy MA;
PI Wood WI;
XX
XX WPI; 2000-452188/39.
DR N-PSDB; AAA46928.
XX
PT New anti-polypeptide antibody useful in the treatment and diagnosis of
PT neoplastic cell growth and proliferation -
XX
XX Claim 61; Fig 18; 220pp; English.
XX
CC The present sequence represents a novel human polypeptide. The
CC specification describes novel polypeptides designated PRO201, PRO292,
CC PRO327, PRO1265, PRO344, PRO343, PRO347, PRO357, PRO715, PRO1017,

CC PRO1112, PRO509, PRO853 and PRO882. These genes are amplified in
CC the genome of tumour cells. The polypeptides are believed to contribute
CC to tumorigenesis. The polypeptides are useful target for the
CC identification of certain cancers, and may act as predictors of the
CC prognosis of tumour treatment. Antibodies against these polypeptides
CC are useful in the treatment and diagnosis of neoplastic cell growth
CC and proliferation in mammals.

XX
SQ Sequence 250 AA;
Query Match 100.0%; Score 1304; DB 21; Length 250;
Best Local Similarity 100.0%; Pred. No. 4.1e-127;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPASSPFLAPKPPGNMGVPREPALSVLWLSWGAALGAVACAMALLTQOTELQSLRR 60
Db 1 MPASSPFLAPKPPGNMGVPREPALSVLWLSWGAALGAVACAMALLTQOTELQSLRR 60
QY 61 EVSRLQGTGSPONGEGYPWQSLPEQSSDALEAWENGERSRKRRAVLTKQKKHSLHL 120
Db 61 EVSRLQGTGSPONGEGYPWQSLPEQSSDALEAWENGERSRKRRAVLTKQKKHSLHL 120
QY 121 VPINATSKDDSDVTEVMQPARLRGRGLQAQGVVRIQDAGVYLLYSQVLPQDVTFTMQQ 180
Db 121 VPINATSKDDSDVTEVMQPARLRGRGLQAQGVVRIQDAGVYLLYSQVLPQDVTFTMQQ 180
QY 181 VVSREGQGRQETLFR CIRSMPSHPDRAYNSCYSAGVFHLHGDILSVIIPRARA KNLSP 240
Db 181 VVSREGQGRQETLFR CIRSMPSHPDRAYNSCYSAGVFHLHGDILSVIIPRARA KNLSP 240
QY 241 HGTFLGFVKL 250
Db 241 HGTFLGFVKL 250

RESULT 6
AAB01323
ID AAB01323 standard; Protein; 250 AA.
XX
AC AAB01323;
XX
DT 25-SEP-2000 (first entry)
XX
DE Human PRO715 polypeptide.
XX
KW PRO; membrane bound protein; secreted protein; PRO357; PRO327;
KW PRO243; PRO715; PRO241; PRO323; PRO299; PRO344; PRO347;
KW PRO355; PRO353; PRO361; transmembrane polypeptide;
KW antibody; screening; detection; inhibition; probe; primer; human.
XX
OS Homo sapiens.

Key Location/Qualifiers
FH Peptide 1..40
FT /label= Signal peptide
FT Domain 34..45
FT /label= Prokaryotic membrane lipoprotein lipid
FT attachment site
FT Modified-site 36..42
FT /note= "N-myristoylation site"
FT Modified-site 40..46
FT /note= "N-myristoylation site"
FT Modified-site 124..128
FT /note= "N-glycosylation site"
FT Modified-site 156..164
FT /note= "Tyrosine kinase phosphorylation site"
FT Modified-site 179..185
FT /note= "N-myristoylation site"
FT Modified-site 242..248
FT /note= "N-myristoylation site"

WO200032776-A2.
XX
PN

PD 08-JUN-2000.
XX
XX
PF 01-DEC-1999; 99WO-US28301.
XX
XX 01-DEC-1998; 98WO-US25108.
PR 16-DEC-1998; 98US-0112850.
PR 22-DEC-1998; 98US-0113296.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;
PI Gerritsen ME, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;
PI Hillan KJ, Kijavini TJ, Napier MA, Roy MA, Tumas D, Wood WI;
XX
DR WPI; 2000-412324/35.
DR N-PSDB; AAAA9565.
XX
PT New human nucleic acids encoding secreted and transmembrane
PT polypeptides, designated as PRO polypeptides, useful as pharmaceutical
PT and diagnostic agents
XX
XX Claim 12; Fig 28; 187pp; English.
XX
XX New human nucleic acids encoding secreted and transmembrane
XX polypeptides which are designated as PRO polypeptides are described
XX The membrane-bound proteins have various industrial applications,
XX including as pharmaceutical and diagnostic agents. The membrane-bound
XX proteins can also be employed for screening of potential peptide or
XX small molecule inhibitors of the relevant receptor/ligand interaction.
XX Anti-PRO antibodies are useful for the affinity purification of PRO
XX from recombinant cell culture or natural sources.
SQ Sequence 250 AA;

Query Match 100.0%; Score 1304; DB 21; Length 250;
Best Local Similarity 100.0%; Pred. No. 4.1e-127;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPASSPFLAPKGPNGMGFPVREPALSVLWLSWGALGAVACAMALLTQOTELQSLRR 60
Db 1 MPASSPFLAPKGPNGMGFPVREPALSVLWLSWGALGAVACAMALLTQOTELQSLRR 60

QY 61 EVSRLOGTGSPSONGEGYPWQSLPEQSSDALLEAWENGERSRKRRAVLTKOKKQHSVLHL 120
Db 61 EVSRLOGTGSPSONGEGYPWQSLPEQSSDALLEAWENGERSRKRRAVLTKOKKQHSVLHL 120

QY 121 VPINATSKDSDVTEVMQPALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQ 180
Db 121 VPINATSKDSDVTEVMQPALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQ 180

QY 181 VVSREGQGRQETLFRICIRSMPSHPDRAYNSCYSGVFLHOGDILSVIIPRARKLNLS 240
Db 181 VVSREGQGRQETLFRICIRSMPSHPDRAYNSCYSGVFLHOGDILSVIIPRARKLNLS 240

QY 241 HGTFLGFVKL 250
Db 241 HGTFLGFVKL 250

RESULT 7
AAE09243
ID AAE09243 standard; Protein; 250 AA.
XX
AC AAE09243;
XX
DT 19-NOV-2001 (first entry)
XX
DE Human APRIL protein.
XX
KW Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor;
KW TNFR; TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis;
KW psoriasis.
XX

XX
OS Homo sapiens.
XX
PN WO200160397-A1.
XX
PD 23-AUG-2001.
XX
PF 28-NOV-2000; 2000WO-US32378.
XX
PR 16-FEB-2000; 2000US-0182938.
PR 22-AUG-2000; 2000US-0226986.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Masters SA, Pitti RM;
PI Yan M;
XX
DR WPI; 2001-541628/60.
DR N-PSDB; AAD15904.
XX
XX Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
PT activity, for treating autoimmune disorders and cancer, comprises
PT exposing the cells to TALL-1 or APRIL polypeptide agonists or
PT antagonists
XX
XX Claim 20; Fig 4; 160pp; English.
XX
XX The invention relates to methods of using one or more agonists or
XX antagonists to modulate the activity of the members of TNF (tumour
XX necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR)
XX e.g. TACI or BCMA. The method is useful for treating pathological
XX conditions or diseases associated with increased TALL-1 and APRIL
XX expression or activity. TALL-1 and APRIL antagonists are used to
XX block the interaction between APRIL and TALL-1 with TACI or BCMA.
XX They are useful for treating a mammal suffering from cancer such
XX as leukaemia, lymphoma, cancers of lung and colon and
XX autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis,
XX psoriasis and lupus erythematosus. The present sequence is human
XX APRIL protein.
SQ Sequence 250 AA;

Query Match 100.0%; Score 1304; DB 22; Length 250;
Best Local Similarity 100.0%; Pred. No. 4.1e-127;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPASSPFLAPKGPNGMGFPVREPALSVLWLSWGALGAVACAMALLTQOTELQSLRR 60
Db 1 MPASSPFLAPKGPNGMGFPVREPALSVLWLSWGALGAVACAMALLTQOTELQSLRR 60

QY 61 EVSRLOGTGSPSONGEGYPWQSLPEQSSDALLEAWENGERSRKRRAVLTKOKKQHSVLHL 120
Db 61 EVSRLOGTGSPSONGEGYPWQSLPEQSSDALLEAWENGERSRKRRAVLTKOKKQHSVLHL 120

QY 121 VPINATSKDSDVTEVMQPALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQ 180
Db 121 VPINATSKDSDVTEVMQPALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQ 180

QY 181 VVSREGQGRQETLFRICIRSMPSHPDRAYNSCYSGVFLHOGDILSVIIPRARKLNLS 240
Db 181 VVSREGQGRQETLFRICIRSMPSHPDRAYNSCYSGVFLHOGDILSVIIPRARKLNLS 240

QY 241 HGTFLGFVKL 250
Db 241 HGTFLGFVKL 250

RESULT 8
AAB62329
ID AAB62329 standard; protein; 250 AA.
XX
AC AAB62329;
XX

DT 29-JUN-2001 (first entry)
XX
DE Human TRDL-1alpha polypeptide.
XX
KW Tumour necrosis factor related death ligand-1gamma; TRDL-1gamma; TRDL;
KW cell death; apoptosis; human; TRDL-1alpha.
XX
OS Homo sapiens.
XX
PN WO200125256-A2.
XX
PD 12-APR-2001.
XX
PF 06-OCT-2000; 2000WO-US27868.
XX
PR 06-OCT-1999; 99US-0157913.
XX
PA (UTAH) UNIV UTAH RES FOUND.
XX
PI Jones D, Manos E;
XX
WPI; 2001-281728/29.
XX
PT Isolated and purified polynucleotide encoding human tumor necrosis
PT factor related death ligand (TRDL)-1 gamma useful for identifying
PT agents that inhibit or enhance TRDL-1 gamma mediated induction of
PT apoptosis -
XX
PS Disclosure; Fig 1; 39pp; English.
XX
CC The invention provides a human tumour necrosis factor related death
CC ligand-1gamma (TRDL-1gamma). The TRDL-1gamma polypeptide can be
CC expressed by standard recombinant methodology. TRDL-1gamma stimulates
CC Jurkat cell death. It is useful for identifying agents capable of
CC inhibiting or enhancing TRDL-1gamma mediated induction of apoptosis.
CC The present sequence represents a TRDL-1alpha polypeptide, used in
CC alignment studies.
XX
SQ Sequence 250 AA;
XX
Query Match 100.0%; Score 1304; DB 22; Length 250;
Best Local Similarity 100.0%; Pred. No. 4.1e-127;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPASSPFLAPKGPFGNMGPVREPALSVLWLSWGALGAVACAMALLTQOTELQSLRR 60
DB 1 MPASSPFLAPKGPFGNMGPVREPALSVLWLSWGALGAVACAMALLTQOTELQSLRR 60
61 EVSRLQGTGSPSQNGEGYPMQSLPEQSSDLEAMENGERSRKRAVLTKQKKQHSVLHL 120
61 EVSRLQGTGSPSQNGEGYPMQSLPEQSSDLEAMENGERSRKRAVLTKQKKQHSVLHL 120
QY 121 VPINATSKDSDVTEVMMPALRRGRGLAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQ 180
DB 121 VPINATSKDSDVTEVMMPALRRGRGLAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQ 180
QY 181 VVSREGQGRQETLFRICIRSMPSHPDRAYNSCYSGAVFHLHOGDILSVIIPRAKLNLS 240
DB 181 VVSREGQGRQETLFRICIRSMPSHPDRAYNSCYSGAVFHLHOGDILSVIIPRAKLNLS 240
QY 241 HGTFLGFVKL 250
DB 241 HGTFLGFVKL 250
RESULT 9
AAV71981
ID AAV71981 standard; Protein: 250 AA.
XX
AC AAV71981;
XX
DT 28-MAR-2001 (first entry)
XX

DE Human TNF and Apol-related Leucocyte-expressed ligand 2/APRIL protein.
XX
XX Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
KW Tumour necrosis factor and Apol-related leucocyte expressed ligand;
KW therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
KW systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
KW thrombocytopenia purpura; acute rheumatic fever; myasthenia gravis;
KW haemolytic anaemia; Grave's disease; Goodpasture's syndrome; TALL2/APRIL;
KW post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA;
KW B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.
XX
OS Homo sapiens.
XX
FH Key
FT Domain
FT 28..48
FT /label= Transmembrane_domain
FT 116..122
FT /label= Beta_strand
FT 138..140
FT /label= Beta_strand
FT 148..150
FT /label= Beta_strand
FT 153..156
FT /label= Beta_strand
FT 162..173
FT /label= Beta_strand
FT 187..192
FT /label= Beta_strand
FT 201..209
FT /label= Beta_strand
FT 210..217
FT /label= Beta_strand
FT 222..230
FT /label= Beta_strand
FT 243..250
FT /label= Beta_strand
XX
XX WO20068378-A1.
XX
PD 16-NOV-2000.
XX
PF 05-MAY-2000; 2000WO-US12266.
XX
PR 06-MAY-1999; 99US-0132892.
PR 01-MAY-2000; 2000US-0201012.
XX
PA (NAJE-) NAT JEWISH MEDICAL & RES CENT.
XX
PI Shu HS;
XX
DR WPI; 2001-016094/02.
XX
PT Isolated TALL-1 protein is used to identify compounds that regulate B
PT lymphocyte proliferation, used to treat B lymphocyte associated
PT autoimmune disorders -
XX
PS Example 1; Fig 1a; 112pp; English.
XX
CC The present invention relates to Tumour necrosis factor (TNF) and
CC Apol-related leucocyte expressed ligand 1 (TALL-1) nucleic acid
CC molecules, proteins (including homologues), and their antibodies. The
CC invention in particular relates to methods for regulating the
CC interaction between TALL-1 and TALL-1 receptors (BCMA referred as B cell
CC maturation factor) to regulate monocyte, macrophage and B lymphocyte
CC mediated immune responses. TALL-1 protein is useful for identifying
CC compounds that regulate B lymphocyte proliferation. It is also useful for
CC treating B lymphocyte associated autoimmune disorders like rheumatoid
CC arthritis, systemic lupus erythematosus (SLE), insulin dependent diabetes
CC mellitus, multiple sclerosis, myasthenia gravis, Grave's disease,
CC autoimmune haemolytic anaemia, autoimmune thrombocytopenia purpura,
CC Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever,
CC post-streptococcal glomerulonephritis, or polyarteritis nodosa.
CC The TALL-1 protein and its corresponding nucleic acid sequence are also

CC useful in diagnostic assays.
CC The present sequence is human Tumour necrosis factor (TNF) and
CC Apol-related leucocyte-expressed ligand 2 (TALL-2)/APRIL protein.
CC TALL-2/APRIL is encoded by the second TNF/FasL like gene. TALL2/APRIL
CC also belongs to the subfamily of TNF family of ligands.

XX Sequence 250 AA;

Query Match 100.0%; Score 1304; DB 22; Length 250;
Best Local Similarity 100.0%; Pred. No. 4.1e-127;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MPASSPFLAPKGPNGMGVREPALSVLWLSWGALGAVACAMALLTQOTELQSLRR 60
DB 1 MPASSPFLAPKGPNGMGVREPALSVLWLSWGALGAVACAMALLTQOTELQSLRR 60
OY 61 EVSRLQGTGSPSQNGEGYPWQSLPEQSSDALEAWENGERSRKRRAVLTKOKKOHSLHL 120
DB 61 EVSRLQGTGSPSQNGEGYPWQSLPEQSSDALEAWENGERSRKRRAVLTKOKKOHSLHL 120
DB 121 VPINATSKDSDVTEVMQPALRRGRGLQAGYGVRIODAGVYLLYSQVLFQDVTFTMGQ 180
DB 121 VPINATSKDSDVTEVMQPALRRGRGLQAGYGVRIODAGVYLLYSQVLFQDVTFTMGQ 180
OY 181 VVSREGQGRQETLFRICIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIPRAKAKLNLS 240
DB 181 VVSREGQGRQETLFRICIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIPRAKAKLNLS 240
OY 241 HGTFLGFVKL 250
DB 241 HGTFLGFVKL 250

RESULT 10
AAU99305
ID AAU99305 standard; Protein; 250 AA.

XX AAU99305;
AC AAU99305;
DT 24-SEP-2002 (first entry)
XX Human tumour necrosis factor ligand (TNFL), TRASH protein #1.
DE Human tumour necrosis factor ligand (TNFL), TRASH protein #1.
XX Human; anti-inflammatory; immunomodulatory; TRASH; TNFL; TANGO 118;
KW tumour necrosis factor ligand; signal transduction; gene therapy;
KW diagnosis; immune response; inflammatory disorder;
KW differentiative disorder; developmental disorder.

Homo sapiens.

XX Key Location/Qualifiers
FT Region 1..44
FT /note= "N-terminal signal transmembrane anchor
FT specifically claimed in claim 27 of the
FT specification"
FT Region 18..250
FT /note= "This region, TRASH protein #2, is specifically
FT claimed in claim 28 of the specification"
FT Region 46..250
FT /note= "This region, TRASH protein #3, is specifically
FT claimed in claim 28 of the specification"
FT Region 50..250
FT /note= "This region, TRASH protein #4, is specifically
FT claimed in claim 28 of the specification"

XX US2002055474-A1.
XX 09-MAY-2002.
XX 27-JAN-1998; 98US-0014348.
XX 27-JAN-1998; 98US-0014348.
XX 27-JAN-1998; 98US-0014348.

PA (BUSF/) BUSFIELD S J.
XX Busfield SJ;
XX WPI; 2002-526818/56.
DR N-PSDB; ABK86985.

PT New nucleic acid encoding a protein designated TRASH is a member of the
PT tumor necrosis factor ligand superfamily of proteins and is useful to
PT detect and treat TRASH-associated disorders including immune and
PT inflammatory disorders

XX Claim 28; Fig 1; 44pp; English.

XX The invention discloses an isolated nucleic acid encoding a novel tumour
XX necrosis factor ligand (TNFL), referred to as TRASH (not defined) (or
XX TANGO 118), protein. Members of the TNFL superfamily are involved in the
XX activation of a large array of cellular genes and of multiple signal
XX transduction pathways, kinases and transcription factors. The nucleic
XX acid and protein can be used in gene therapy, to identify compounds that
XX modulates TRASH activity, raise antibodies and treat, or diagnose,
XX disorders associated with aberrant TRASH activity or expression,
XX particularly an immune response or inflammatory disorder, or a
XX differentiative or developmental disorder. The sequence presented is the
XX human tumour necrosis factor ligand (TNFL), TRASH protein #1.

XX Sequence 250 AA;

Query Match 100.0%; Score 1304; DB 23; Length 250;
Best Local Similarity 100.0%; Pred. No. 4.1e-127;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MPASSPFLAPKGPNGMGVREPALSVLWLSWGALGAVACAMALLTQOTELQSLRR 60
DB 1 MPASSPFLAPKGPNGMGVREPALSVLWLSWGALGAVACAMALLTQOTELQSLRR 60
OY 61 EVSRLQGTGSPSQNGEGYPWQSLPEQSSDALEAWENGERSRKRRAVLTKOKKOHSLHL 120
DB 61 EVSRLQGTGSPSQNGEGYPWQSLPEQSSDALEAWENGERSRKRRAVLTKOKKOHSLHL 120
OY 121 VPINATSKDSDVTEVMQPALRRGRGLQAGYGVRIODAGVYLLYSQVLFQDVTFTMGQ 180
DB 121 VPINATSKDSDVTEVMQPALRRGRGLQAGYGVRIODAGVYLLYSQVLFQDVTFTMGQ 180
OY 181 VVSREGQGRQETLFRICIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIPRAKAKLNLS 240
DB 181 VVSREGQGRQETLFRICIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIPRAKAKLNLS 240
OY 241 HGTFLGFVKL 250
DB 241 HGTFLGFVKL 250

RESULT 11
ABB81486
ID ABB81486 standard; Protein; 250 AA.

XX ABB81486;
AC ABB81486;
DT 02-SEP-2002 (first entry)
XX Human ZTNF2 amino acid sequence SEQ ID NO:6.

XX Human; Ztnfr12; tumour necrosis factor receptor; cytostatic;
KW immunosuppressive; dermatological; antiinflammatory; antidiabetic;
KW neuroprotective; antirheumatic; antiarthritic; antiasthmatic;
KW nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;
KW autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;
KW multiple sclerosis; insulin dependent diabetes mellitus; asthma;
KW rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;
KW glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;
KW pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis;
KW light chain neuropathy; hypertension; large vessel disease;

KW graft-versus host disease; graft rejection; Crohn's disease.
XX Homo sapiens.
XX WO200238766-A2.
XX 16-MAY-2002.
XX 05-NOV-2001; 2001WO-US47018.
XX 07-NOV-2000; 2000US-246449P.
PR 20-DEC-2000; 2000US-257131P.
PR 28-JUN-2001; 2001US-301715P.
PR 29-AUG-2001; 2001US-315565P.
XX (ZYMO) ZYMOGENETICS INC.
XX Gross JA, Xu W, Henne RM, Grant FJ;
PI WPI; 2002-508212/54.
PT Novel isolated human tumor necrosis factor receptor polypeptide, termed
PT Ztnfr 12, useful for treating autoimmune disorders, emphysema, end
PT stage renal failure or renal disease and lymphoma
XX Disclosure; Page 135; 154pp; English.
XX The present invention describes a human tumor necrosis factor receptor
CC designated Ztnfr12 (I). (I) has cytostatic, immunosuppressive,
CC dermatological, antiinflammatory, neuroprotective, antidiabetic,
CC antirheumatic, antiarthritic, antiaslathmatic, nephrotropic and hypotensive
CC activities, and can be used in gene therapy. (I) can be used for
CC inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12
CC (e.g. ZTNF4), for treating disorders and diseases associated with B
CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
CC inhibiting the proliferation of tumour cells. (I) is useful for treating
CC autoimmune disorders such as systemic lupus erythematosus, myasthenia
CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
CC leukaemia, nephritis, and pyelonephritis, and for treating renal
CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or
CC amyloidosis, hypertension, large vessel diseases, graft-versus host
CC disease, graft rejection and Crohn's disease. (I) is useful for
CC modulating the immune system, for regulating B cell responses and
CC development, for modulating development of other cells, antibody
CC production and cytokine production, and for modulating T and B cell
CC communication. The present sequence represents the human ZTNF2 protein
CC which is given in the exemplification of the present invention.
SQ Sequence 250 AA;
Query Match 100.0%; Score 1304; DB 23; Length 250;
Best Local Similarity 100.0%; Pred. No. 4.1e-127;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 241 HGTFGLGVKL 250
|||||
RESULT 12
ABP47228
ID ABP47228 standard; Protein; 250 AA.
XX
XX AC ABP47228;
XX 19-AUG-2002 (first entry)
XX DT
XX DE Human Blys binding scFv VH CDR3 SEQ ID 3239.
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
XX OS Homo sapiens.
XX PN WO200202641-A1.
XX 10-JAN-2002.
XX PD
XX PF 15-JUN-2001; 2001WO-US19110.
XX PR 16-JUN-2000; 2000US-212210P.
PR 17-OCT-2000; 2000US-240816P.
PR 16-MAR-2001; 2001US-276248P.
PR 21-MAR-2001; 2001US-277379P.
PR 25-MAY-2001; 2001US-293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
DR
XX
XX PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for
PT the diagnosis and treatment of cancers and immune disorders -
XX
XX PS Disclosure; Page 3147-3148; 3148pp; English.
XX
XX CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method
CC of the invention.
XX
SQ Sequence 250 AA;
Query Match 100.0%; Score 1304; DB 23; Length 250;
Best Local Similarity 100.0%; Pred. No. 4.1e-127;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPASSPFLAPKPGPGNMGPVREPALSVALLWSGALGAVACAMALLTQOTELQSLRR 60
|||||

Db 1 MPASSPFLAPKPPGPMGVPVREPALSVALWLSWGALGAVACAMALLTQOTELQSLRR 60
Qy 61 EVSRLQGTGSPSQNGEGYPWQSLPEQSSDALAEWENGERSRKRRAVLTQKKOHSLVHL 120
Db 61 EVSRLQGTGSPSQNGEGYPWQSLPEQSSDALAEWENGERSRKRRAVLTQKKOHSLVHL 120
Qy 121 VPINATSKDSDVTEVMQPALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQ 180
Db 121 VPINATSKDSDVTEVMQPALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQ 180
Qy 181 VVSREGQGRQETLFRICRSMPSHPDRAYNSCYSAGVFHLHOGDILSVIIPRAKLNLS 240
Db 181 VVSREGQGRQETLFRICRSMPSHPDRAYNSCYSAGVFHLHOGDILSVIIPRAKLNLS 240
Qy 241 HGTFLGFWKL 250
Db 241 HGTFLGFWKL 250

ULT 13
ID AAV79155 standard; Protein; 250 AA.
XX AAU79155;
AC AAU79155;
XX
DT 02-JUL-2002 (first entry)
XX
DE Human APRIL (a proliferation-inducing ligand) protein #2.
XX
KW Human; Neutrokin-alpha; antibody; immunogen; B-cell cancer;
KW autoimmune disease; Sjogren's syndrome; systemic lupus erythematosus;
KW rheumatoid arthritis; chronic lymphocytic leukaemia; multiple myeloma;
KW Hodgkin's lymphoma; non-Hodgkin's lymphoma; hypergammaglobulinemia;
KW APRIL; a proliferation-inducing ligand.
XX
OS Homo sapiens.
XX
PN WO200218620-A2.
XX
PD 07-MAR-2002.
XX
PF 15-AUG-2001; 2001WO-US25549.
XX
PR 15-AUG-2000; 2000US-225628P.
PR 23-AUG-2000; 2000US-227008P.
PR 22-SEP-2000; 2000US-234338P.
PR 17-OCT-2000; 2000US-240806P.
PR 30-NOV-2000; 2000US-250020P.
PR 06-MAR-2001; 2001US-276248P.
PR 25-MAY-2001; 2001US-293499P.
PR 07-JUN-2001; 2001US-296122P.
PR 13-JUL-2001; 2001US-304809P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Yu G, Ebner R, Ni J, Rosen CA, Ulrich S;
XX
DR WPI; 2002-304259/34.
XX
XX An isolated antibody or portion that specifically binds to a protein
PT useful in the treatment of diseases such as hypergammaglobulinemia and
PT cancer -
XX
PS Claim 1; Page 481-482; 482pp; English.
XX
XX The present invention relates to a new antibody, or portion, that
CC specifically binds to a protein which has a 285 or 250 amino acid
CC sequence as fully defined in the specification. The antibody of the
CC invention is useful in treating a disease or disorder such as cancer,
CC especially B-cell cancer, autoimmune diseases such as Sjogren's
CC syndrome, systemic lupus erythematosus, rheumatoid arthritis, chronic
CC lymphocytic leukaemia, multiple myeloma, Hodgkin's lymphoma,
CC non-Hodgkin's lymphoma or hypergammaglobulinemia, or in diagnosing a

CC disease or disorder comprising assaying expression of Neutrokin-alpha
CC and APRIL (a proliferation-inducing ligand) in cells or body fluids using
CC antibodies and comparing the Neutrokin-alpha and APRIL expression level
CC with a standard Neutrokin-alpha and APRIL expression level, whereby an
CC increase or decrease in the assayed Neutrokin-alpha and APRIL expression
CC level compared to the standard levels is indicative of a disease or
CC disorder. The present amino acid sequence represents the human APRIL
CC protein #2 of the invention.
XX
SQ Sequence 250 AA;
Query Match 100.0%; Score 1304; DB 23; Length 250;
Best Local Similarity 100.0%; Pred. No. 4,1e-127;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPASSPFLAPKPPGPMGVPVREPALSVALWLSWGALGAVACAMALLTQOTELQSLRR 60
Db 1 MPASSPFLAPKPPGPMGVPVREPALSVALWLSWGALGAVACAMALLTQOTELQSLRR 60
Qy 61 EVSRLQGTGSPSQNGEGYPWQSLPEQSSDALAEWENGERSRKRRAVLTQKKOHSLVHL 120
Db 61 EVSRLQGTGSPSQNGEGYPWQSLPEQSSDALAEWENGERSRKRRAVLTQKKOHSLVHL 120
Qy 121 VPINATSKDSDVTEVMQPALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQ 180
Db 121 VPINATSKDSDVTEVMQPALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQ 180
Qy 181 VVSREGQGRQETLFRICRSMPSHPDRAYNSCYSAGVFHLHOGDILSVIIPRAKLNLS 240
Db 181 VVSREGQGRQETLFRICRSMPSHPDRAYNSCYSAGVFHLHOGDILSVIIPRAKLNLS 240
Qy 241 HGTFLGFWKL 250
Db 241 HGTFLGFWKL 250

RESULT 14
AAW93588
ID AAW93588 standard; Protein; 250 AA.
XX
AC AAW93588;
XX
DT 18-JUN-1999 (first entry)
XX
DE Human TNRL1-beta protein.
XX
KW Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
KW developmental abnormality; gestational abnormality; prostate cancer;
KW APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
KW cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
KW apoptosis; human; TNRL1-beta.
XX
OS Homo sapiens.
XX
PN WO9911791-A2.
XX
PD 11-MAR-1999.
XX
PF 04-SEP-1998; 98WO-US18393.
XX
PR 05-SEP-1997; 97US-0924634.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Chaudhary PM;
XX
DR WPI; 1999-205191/17.
XX
XX N-PSDB; AAX23422.
XX
XX New Tumour Necrosis Factor family receptor polypeptides and ligands -
PT useful for diagnosis and treatment of prostate cancer and
PT developmental or gestational abnormalities
XX

